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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 03:09:31 ; Search time 886 Seconds
(without alignments)
11458.669 Million cell updates/sec

Title: US-10-086-623-5
Perfect score: 1934
Sequence: 1 ttgtaccgaagatgagac.....atcgacgtaactggaaccg 1934

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description |
|------------|--------|---------------|--------|----|----------|--------------------|
| 1 | 1934 | 100.0 | 1934 | 3 | AAD00737 | Aad00737 Human Pla |
| 2 | 1934 | 100.0 | 2253 | 3 | AAD00738 | Aad00738 Human Pla |
| 3 | 1934 | 100.0 | 2253 | 8 | ABQ80246 | Abq80246 PDGF-D CD |
| 4 | 1913.6 | 98.9 | 4001 | 5 | AAH46957 | Aah46957 Human sec |
| 5 | 1913.6 | 98.9 | 4001 | 6 | ABS58493 | Abs58493 Human sec |
| 6 | 1913.2 | 98.9 | 3739 | 10 | ADG65192 | Adg65192 Cell prol |
| 7 | 1913.2 | 98.9 | 3808 | 12 | ADO20112 | Ado20112 Human PRO |
| 8 | 1911.6 | 98.8 | 3798 | 5 | AAH46939 | Aah46939 Human sec |
| 9 | 1911.6 | 98.8 | 3798 | 6 | ABS58475 | Abs58475 Human sec |
| 10 | 1903.6 | 98.4 | 3718 | 6 | AAD25489 | Aad25489 Human LP8 |
| 11 | 1903.6 | 98.4 | 3736 | 6 | AAD25488 | Aad25488 Human LP8 |
| 12 | 1902.8 | 98.4 | 3853 | 4 | AAF24196 | Aaf24196 Human VEG |
| 13 | 1896.2 | 98.0 | 4153 | 12 | ADQ23870 | Adq23870 Human sof |
| 14 | 1896.2 | 98.0 | 4153 | 12 | ADQ22990 | Adq22990 Human sof |
| 15 | 1896.2 | 98.0 | 4153 | 12 | ADQ24013 | Adq24013 Human sof |
| 16 | 1518.8 | 78.5 | 1587 | 4 | AAS04493 | Aas04493 Human FCT |
| 17 | 1518.8 | 78.5 | 1587 | 6 | ABN84525 | Abn84525 Human FCT |
| 18 | 1518.8 | 78.5 | 1587 | 6 | ABS63516 | Abs63516 Human FCT |
| 19 | 1518.8 | 78.5 | 1587 | 10 | ADK68111 | Adk68111 Novel NOV |
| 20 | 1517.2 | 78.4 | 1587 | 10 | ADK68131 | Adk68131 Novel NOV |
| 21 | 1517.2 | 78.4 | 1587 | 10 | ADK68125 | Adk68125 Novel NOV |

| | | | | | | |
|----|--------|------|------|----|----------|--------------------|
| 22 | 1517.2 | 78.4 | 1587 | 10 | ADK68123 | Adk68123 Novel NOV |
| 23 | 1517.2 | 78.4 | 1587 | 10 | ADK68133 | Adk68133 Novel NOV |
| 24 | 1517.2 | 78.4 | 1587 | 10 | ADK68135 | Adk68135 Novel NOV |
| 25 | 1517.2 | 78.4 | 1587 | 10 | ADK68129 | Adk68129 Novel NOV |
| 26 | 1517.2 | 78.4 | 1587 | 12 | ADM57644 | Adm57644 Human FCT |
| 27 | 1505.2 | 77.8 | 1586 | 10 | ADK68127 | Adk68127 Novel NOV |
| 28 | 1501.4 | 77.6 | 1728 | 4 | AAS04498 | Aas04498 Human PDG |
| 29 | 1501.4 | 77.6 | 1828 | 4 | AAS04492 | Aas04492 Human FCT |
| 30 | 1501.4 | 77.6 | 1828 | 6 | ABN84524 | Abn84524 Human FCT |
| 31 | 1501.4 | 77.6 | 1828 | 6 | ABS63515 | Abs63515 Human FCT |
| 32 | 1501.4 | 77.6 | 1828 | 10 | ADK18626 | Adk18626 Human PDG |
| 33 | 1498.2 | 77.5 | 1828 | 12 | ADM57642 | Adm57642 Human FCT |
| 34 | 1491.8 | 77.1 | 1882 | 3 | AAAS1541 | Aaa51541 SEQ. ID. |
| 35 | 1491.8 | 77.1 | 1882 | 3 | AAC81555 | Aac81555 Human gro |
| 36 | 1491.8 | 77.1 | 1882 | 4 | AAH47772 | Aah47772 Human zve |
| 37 | 1491.8 | 77.1 | 1882 | 6 | ABS68643 | Abs68643 Human cDN |
| 38 | 1491.8 | 77.1 | 1882 | 6 | ABN84420 | Abn84420 Human zve |
| 39 | 1491.8 | 77.1 | 1882 | 6 | ABQ73239 | Abq73239 Human zve |
| 40 | 1491.8 | 77.1 | 1882 | 8 | ABX93177 | Abx93177 DNA encod |
| 41 | 1491.8 | 77.1 | 1882 | 8 | ACC47941 | Acc47941 Human PDG |
| 42 | 1491.8 | 77.1 | 1882 | 9 | AAD58378 | Aad58378 Human pla |
| 43 | 1491.8 | 77.1 | 1882 | 10 | AAD64615 | Aad64615 Human zve |
| 44 | 1491.8 | 77.1 | 1882 | 10 | ADG47745 | Adg47745 Human zve |
| 45 | 1491.8 | 77.1 | 1882 | 10 | ACA64109 | Aca64109 Human cDN |

ALIGNMENTS

RESULT 1
AAD00737
ID AAD00737 standard; cDNA; 1934 BP.
XX
AC AAD00737;
XX
DT 08-SEP-2000 (first entry)
XX
DE Human Platelet Derived Growth Factor (PDGF)-D encoding partial cDNA #2.
XX
KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary;
KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
KW proliferative; activator; proliferation; differentiation; motility;
KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
KW atherosclerosis; wound; metastasis; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 1..969
FT /*tag= a
FT /partial
FT /product= "Human PDGF-D partial polypeptide #2"
FT /note= "5' truncated platelet derived growth factor"

WO200027879-A1.

18-MAY-2000.

10-NOV-1999; 99WO-US026462.

10-NOV-1998; 98US-0107852P.

28-DEC-1998; 98US-0113997P.

26-AUG-1999; 99US-0150604P.

04-OCT-1999; 99US-0157108P.

05-OCT-1999; 99US-0157756P.

(LUDW-) LUDWIG INST CANCER RES.

(UYHE-) UNIV HELSINKI LICENSING LTD OY.

Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;

Oestman A, Heldin C;

WPI; 2000-376495/32.

DR P-PSDB; AAY71129.

XX Novel polynucleotides encoding a novel growth factor of cells expressing

PT a platelet-derived growth factor, useful for diagnostic and therapeutic

PT applications, e.g. concerning cancer.

XX

PS Claim 1; Fig 5; 111pp; English.

XX

CC The present sequence is the 5' truncated partial cDNA #2, encoding human

CC platelet derived growth factor (PDGF)-D, formally known as Vascular

CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung

CC lambdaagt10 cDNA library. It belongs to the VEGF/PDGF family. It functions

CC as an activator of proliferation, differentiation, growth and motility of

CC cells, that express PDGF-D receptor. This sequence is useful for

CC inhibiting the growth of tumours, that express PDGF-D. Expression of PDGF

CC -D and its proteolytic cleavage for generating an activated truncated

CC form is useful for regulating receptor binding specificity of PDGF-D.

CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the

CC invasion of tumour cells into normal cells. PDGF-D may be used to treat

CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells

XX

SQ Sequence 1934 BP; 632 A; 366 C; 394 G; 542 T; 0 U; 0 Other;

Query Match 100.0%; Score 1934; DB 3; Length 1934;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1934; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCTCTAGA 60

DB |||||||

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCTCTAGA 60

DB |||||||

QY 61 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAAT 120

DB |||||||

QY 61 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAAT 120

DB |||||||

QY 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180

DB |||||||

QY 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180

DB |||||||

QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 240

DB |||||||

QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 240

DB |||||||

QY 241 CGATGGTGTGGACACAAAGGAAGTTCCCTCAAGGATAAAATCAAGAACGAACCAAATTAA 300

DB |||||||

QY 241 CGATGGTGTGGACACAAAGGAAGTTCCCTCAAGGATAAAATCAAGAACGAACCAAATTAA 300

DB |||||||

QY 301 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 360

DB |||||||

QY 301 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 360

DB |||||||

QY 361 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 420

DB |||||||

QY 361 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 420

DB |||||||

QY 421 TCTATTTTCAAGGGTATCCCTATAACTCTCCATCAGTAACGGATCCCACCTCTGATTGCGGAT 480

DB |||||||

QY 421 TCTATTTTCAAGGGTATCCCTATAACTCTCCATCAGTAACGGATCCCACCTCTGATTGCGGAT 480

DB |||||||

QY 481 GCTCTGGACAAAAAATTGCAGAATTTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 540

DB |||||||

QY 481 GCTCTGGACAAAAAATTGCAGAATTTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 540

DB |||||||

QY 541 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 600

DB |||||||

QY 541 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 600

DB |||||||

QY 601 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGCCAAG 660

DB |||||||

QY 601 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGCCAAG 660

DB |||||||

QY 661 CGTTACAGTTGCACCTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 720

DB |||||||

Db 661 CGTTACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAAGAGCTGAAGTTGGCC 720

QY 721 AATGTGGTCTTCTTTCCACGTTGCTCCTCCTCGTGACGGCTGTGGAGGAATTTGTGGCTGT 780

Db |||||||

Db 721 AATGTGGTCTTCTTTCCACGTTGCTCCTCCTCGTGACGGCTGTGGAGGAATTTGTGGCTGT 780

QY 781 GGAACCTGTCAACTGGAGGTCTCTGCACATGCAATTCAGGGAAACCCGTGAAAAAGTATCAT 840

Db |||||||

Db 781 GGAACCTGTCAACTGGAGGTCTCTGCACATGCAATTCAGGGAAACCCGTGAAAAAGTATCAT 840

QY 841 GAGGTATTACAGTTTGAAGCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900

Db |||||||

Db 841 GAGGTATTACAGTTTGAAGCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900

QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 960

Db |||||||

Db 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 960

QY 961 CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020

Db |||||||

Db 961 CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020

QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAACTTACTACTAGCCTGCAATGCA 1080

Db |||||||

Db 1021 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAACTTACTACTAGCCTGCAATGCA 1080

QY 1081 ATGAACACAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1140

Db |||||||

Db 1081 ATGAACACAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1140

QY 1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCAATTTAATAATAGTTTGG 1200

Db |||||||

Db 1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCAATTTAATAATAGTTTGG 1200

QY 1201 GTTATATATGCAAAAAACACACACAGAAATATATTATGCTATGTGTATATAGATCAAAAT 1260

Db |||||||

Db 1201 GTTATATATGCAAAAAACACACACAGAAATATATTATGCTATGTGTATATAGATCAAAAT 1260

QY 1261 GTTTTTTTTGGTATATATAAACCAGGTACACAGAGCTTACATATGTTGAGTTAGACTCT 1320

Db |||||||

Db 1261 GTTTTTTTTGGTATATATAAACCAGGTACACAGAGCTTACATATGTTGAGTTAGACTCT 1320

QY 1321 TAAAAATCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGCTTTTAGAAAAATTT 1380

Db |||||||

Db 1321 TAAAAATCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGCTTTTAGAAAAATTT 1380

QY 1381 AGGAGATAAATTTATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGCTCTCTTA 1440

Db |||||||

Db 1381 AGGAGATAAATTTATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGCTCTCTTA 1440

QY 1441 AAGAAAGCATCTTGTATATTAAAAATCAAAAGATGAGGCTTTTACATATACATCTTAG 1500

Db |||||||

Db 1441 AAGAAAGCATCTTGTATATTAAAAATCAAAAGATGAGGCTTTTACATATACATCTTAG 1500

QY 1501 TTGATTATTAAAAAAGGAAAAAGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTTTTTC 1560

Db |||||||

Db 1501 TTGATTATTAAAAAAGGAAAAAGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTTTTTC 1560

QY 1561 CATGAGAAGCATGTCATACCTTACCTATGTGGACTGTAATAACCTGTCTCCAAAAACCATGC 1620

Db |||||||

Db 1561 CATGAGAAGCATGTCATACCTTACCTATGTGGACTGTAATAACCTGTCTCCAAAAACCATGC 1620

QY 1621 CATAATAATAAGTGTCTTTAGAAATTAATCATTTGTTTTTTTATGCAATTTTGTGAGG 1680

Db |||||||

Db 1621 CATAATAATAAGTGTCTTTAGAAATTAATCATTTGTTTTTTTATGCAATTTTGTGAGG 1680

QY 1681 CATCCTTATTCAATTTAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTTTATTATAGTC 1740

Db |||||||

Db 1681 CATCCTTATTCAATTTAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTTTATTATAGTC 1740

QY 1741 CTACAAAAGACAATGTATAAGCTGTAAACAGAAATTTTGAATTTTCTTTTGCAAAACCC 1800

Db |||||||

Db 1741 CTACAAAAGACAATGTATAAGCTGTAAACAGAAATTTTGAATTTTCTTTTGCAAAACCC 1800

Db 1220 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 1279

QY 961 CCTCGATAAGAGAATGTGCACATCCTTACATTAAAGCCTGAAAGAACCTTTTAGTTTAAGGA 1020

Db 1280 CCTCGATAAGAGAATGTGCACATCCTTACATTAAAGCCTGAAAGAACCTTTTAGTTAAGGA 1339

QY 1021 GGGTGAGATAAGAGACCCCTTTTCTTACCAGCAACCAAACTTACTACTAGCCCTGCAATGCA 1080

Db 1340 GGGTGAGATAAGAGACCCCTTTTCTTACCAGCAACCAAACTTACTACTAGCCCTGCAATGCA 1399

QY 1081 ATGAACACAAAGTGGTGTGAGTCTCAGCCTTGCTTTGTTTAATGCCATGGCAAGTAGAAA 1140

Db 1400 ATGAACACAAAGTGGTGTGAGTCTCAGCCTTGCTTTGTTTAATGCCATGGCAAGTAGAAA 1459

QY 1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCATTTAATAATAGTGTGAG 1200

Db 1460 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCATTTAATAATAGTGTGAG 1519

QY 1201 GTTATATATGCACAAAACACACACAGAAATATATTCAATGTCTATGTGTATATAGATCAAA 1260

Db 1520 GTTATATATGCACAAAACACACAGAAATATATTCAATGTCTATGTGTATATAGATCAAA 1579

QY 1261 GTTTTTTTTGGTATATATAAACCCAGGTACACCAGATTACATATGTTTGAGTTAGACTCT 1320

Db 1580 GTTTTTTTTGGTATATATAAACCCAGGTACACCAGATTACATATGTTTGAGTTAGACTCT 1639

QY 1321 TAAAAATCCTTTGCCAAAATAAAGGGATGGTCAAAATATATGAAACATGCTTTTAGAAAAATTT 1380

Db 1640 TAAAAATCCTTTGCCAAAATAAAGGGATGGTCAAAATATATGAAACATGCTTTTAGAAAAATTT 1699

QY 1381 AGGAGATAAAATTTATTTTAAATTTTGAAACACAAAACAATTTTGAATCTTGCTCTCTTA 1440

Db 1700 AGGAGATAAAATTTATTTTAAATTTTGAAACACAAAACAATTTTGAATCTTGCTCTCTTA 1759

QY 1441 AAGAAAGCATCTTGATATATAAAAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG 1500

Db 1760 AAGAAAGCATCTTGATATATAAAAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG 1819

QY 1501 TTGATTATTAAAAAAGGAAAAAGGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTTTC 1560

Db 1820 TTGATTATTAAAAAAGGAAAAAGGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTTTC 1879

QY 1561 CATGAGAAAGCACTGCATACTTACCTATGTGGACTGTAAATAACCTGTCTCCAAAACCATGC 1620

Db 1880 CATGAGAAAGCACTGCATACTTACCTATGTGGACTGTAAATAACCTGTCTCCAAAACCATGC 1939

QY 1621 CATAATAATATAAGTGCTTTAGAAAATTAATCAATGTGTTTTTATGCAATTTTGTGAGG 1680

Db 1940 CATAATAATATAAGTGCTTTAGAAAATTAATCAATGTGTTTTTATGCAATTTTGTGAGG 1999

QY 1681 CATCCTTATTTCATTTAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTTTATATAGTC 1740

Db 2000 CATCCTTATTTCATTTAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTTTATATAGTC 2059

QY 1741 CTACAAAAGACAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTTCTTTGCAAAACCC 1800

Db 2060 CTACAAAAGACAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTTCTTTGCAAAACCC 2119

QY 1801 CTCCACAAAAGCAAATCCTTTCAAGAAATGGCATGGCATCTGTATGAACCTTTCCAGAT 1860

Db 2120 CTCCACAAAAGCAAATCCTTTCAAGAAATGGCATGGCATCTGTATGAACCTTTCCAGAT 2179

QY 1861 GGTGTTTCAGTGAAAGATGTGGGTAGTTGAGAACTTTAAAAAGTGAACATTTGAACATCGAC 1920

Db 2180 GGTGTTTCAGTGAAAGATGTGGGTAGTTGAGAACTTTAAAAAGTGAACATTTGAACATCGAC 2239

QY 1921 GTAACCTGGAAACCG 1934

Db 2240 GTAACCTGGAAACCG 2253

ID XX ABQ80246 standard; cDNA; 2253 BP.

AC XX ABQ80246;

DT XX 27-JUN-2003 (first entry)

DE XX PDGF-D cDNA.

DE XX Gene; nervous system; platelet-derived growth factor; PDGF; psychosis;

KW vascular endothelial growth factor; VEGF; neural; stem cell; memory;

KW progenitor cell; neurodegeneration; ischaemia; neurological trauma;

KW neuropsychiatry; learning; Parkinson's disease; Huntington's disease;

KW Amyotrophic Lateral Sclerosis; spinal ischaemia; ischaemic stroke;

KW spinal cord injury; cancer-related; schizophrenia; Alzheimer's disease;

KW depression; anxiety; phobia; stress; cognitive function; aggression;

KW drug; alcohol; abuse; obsessive compulsive behaviour; proliferation;

KW seasonal mood disorder; personality disorder; cerebral palsy;

KW multi-infarct; dementia; Lewy body; age related; geriatric; growth;

KW epilepsy; brain injury; multiple sclerosis; autism; differentiation;

XX attention deficit disorder; narcolepsy; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FH CDS .176..1288

FT /*tag= a

FT /product= "PDGF-D"

XX WO2003024478-A1.

XX 27-MAR-2003.

XX 19-SEP-2002; 2002WO-IB003998.

PR 19-SEP-2001; 2001US-0323381P.

PR 28-SEP-2001; 2001US-0326044P.

XX (NEUR-) NEURONOVA AB.

PA Delfani K, Janson AM, Kuhn GH, Plate K, Schanzer A, Wachs F;

PI Zhao M;

XX WPI; 2003-354563/33.

DR P-PSDB; ABB80134.

XX Use of platelet-derived growth factor, vascular endothelial growth

PT factor, or their modulators for modulating neural stem cell or neural

PT progenitor cell activity, particularly for treating e.g. Alzheimer's,

PT ischemia or stroke.

XX Claim 97; Page 22-23; 119pp; English.

PS The sequences given in ABQ80243-47 encode proteins which may be used in

XX the method of the invention for alleviating or reducing a symptom of a

CC disease or disorder of the nervous system. The method comprises

CC administering platelet-derived growth factor (PDGF), vascular endothelial

CC growth factor (VEGF), a combination of PDGF and VEGF, or a PDGF or VEGF

CC agonist, to a patient in order to modulate neural stem cell or neural

CC progenitor cell activity in vivo. The method is useful for alleviating or

CC reducing the symptoms of a disease or disorder of the nervous system,

CC e.g. neurodegenerative disorders, neural stem cell disorders, neural

CC progenitor disorders, ischaemic disorders, neurological traumas,

CC affective disorders, neuropsychiatric disorders or learning and memory

CC disorders. In particular, the method is useful for alleviating or

CC treating Parkinson's disease and disorders, Huntington's disease,

CC Alzheimer's disease, Amyotrophic Lateral Sclerosis, spinal ischaemia,

CC ischaemic stroke, spinal cord injury or cancer-related brain/ spinal cord

CC injury, schizophrenia and other psychoses, depression, bipolar

CC depression/disorder, anxiety syndromes/disorders, phobias, stress and

CC related syndromes, cognitive function disorders, aggression, drug and

CC alcohol abuse, obsessive compulsive behaviour syndromes, seasonal mood

CC disorder, borderline personality disorder, cerebral palsy, life style

CC drug, multi-infarct dementia, Lewy body dementia, age related/geriatric

| | |
|---|--|
| CC | dementia, epilepsy and injury related to epilepsy, spinal cord injury, brain injury, trauma related brain/spinal cord injury, anti-cancer |
| CC | treatment related brain/spinal cord tissue injury, infection and inflammation related brain/spinal cord injury, environmental toxin |
| CC | related brain/spinal cord injury, multiple sclerosis, autism, attention deficit disorders, narcolepsy or sleep disorders. The PDGF and/or VEGF, is useful in the manufacture of a medicament for alleviating or treating these diseases or disorders, accelerating growth of neural stem cells or neural progenitor cells, or inducing proliferation or differentiation of these cells |
| XX | |
| SQ | Sequence 2253 BP; 701 A; 464 C; 490 G; 598 T; 0 U; 0 Other; |
| Query Match 100.0%; Score 1934; DB 8; Length 2253; | |
| Best Local Similarity 100.0%; Pred. No. 0; | |
| Matches 1934; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Qy | 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGAGAGTCCTAGA 60 |
| Db | |
| 320 | TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGAGAGTCCTAGA 379 |
| Qy | 61 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 120 |
| Db | |
| 380 | TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 439 |
| Qy | 121 ACACGGATACAGCTAGTGTGTTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180 |
| Db | |
| 440 | ACACGGATACAGCTAGTGTGTTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 499 |
| Qy | 181 TGTAGGTATGATTTGTGGAAAGTTGAAGATATATCCGAAACCAAGTACCATTATTAGAGGA 240 |
| Db | |
| 500 | TGTAGGTATGATTTGTGGAAAGTTGAAGATATATCCGAAACCAAGTACCATTATTAGAGGA 559 |
| Qy | 241 CGATGGTGTGGACAAAGGAAGTTCCCTCCAGGATAAAATCAAGAACGAACCAAAATTAA 300 |
| Db | |
| 560 | CGATGGTGTGGACAAAGGAAGTTCCCTCCAGGATAAAATCAAGAACGAACCAAAATTAA 619 |
| Qy | 301 ATCACATTCAAGTCGATGACTACTTTGTGGCTPAAACCTGGATTCAAGATTTATTCT 360 |
| Db | |
| 620 | ATCACATTCAAGTCGATGACTACTTTGTGGCTPAAACCTGGATTCAAGATTTATTCT 679 |
| Qy | 361 TTGCTGGAAGATTTCCAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCACAAGC 420 |
| Db | |
| 680 | TTGCTGGAAGATTTCCAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCACAAGC 739 |
| Qy | 421 TCTATTTCCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480 |
| Db | |
| 740 | TCTATTTCCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 799 |
| Qy | 481 GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 540 |
| Db | |
| 800 | GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 859 |
| Qy | 541 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 600 |
| Db | |
| 860 | CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 919 |
| Qy | 601 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660 |
| Db | |
| 920 | AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 979 |
| Qy | 661 CGTTACAGTTGCACCTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 720 |
| Db | |
| 980 | CGTTACAGTTGCACCTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 1039 |
| Qy | 721 AATGTGGTCTTCTTTCCAGCTTGCCTCCTCGTGACGGCTGTGGAGGAATTGTGGCTGT 780 |
| Db | |
| 1040 | AATGTGGTCTTCTTTCCAGCTTGCCTCCTCGTGACGGCTGTGGAGGAATTGTGGCTGT 1099 |
| Qy | 781 GGAACGTGTCAGGTCTGACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 840 |
| Db | |
| 1100 | GGAACGTGTCAGGTCTGACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 1159 |

| | |
|------|--|
| Qy | 841 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900 |
| Db | |
| 1160 | GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 1219 |
| Qy | 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 960 |
| Db | |
| 1220 | CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 1279 |
| Qy | 961 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTAAGGA 1020 |
| Db | |
| 1280 | CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTAAGGA 1339 |
| Qy | 1021 GGGTGAGATAAGAGACCCCTTTTCCCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1080 |
| Db | |
| 1340 | GGGTGAGATAAGAGACCCCTTTTCCCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1399 |
| Qy | 1081 ATGAACACAAAGTGTGCTGAGTCTCAGSCTTGCTTTGTTAAATGCCATGGCAAGTAGAAA 1140 |
| Db | |
| 1400 | ATGAACACAAAGTGTGCTGAGTCTCAGSCTTGCTTTGTTAAATGCCATGGCAAGTAGAAA 1459 |
| Qy | 1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCAATTTAATAATAGTGTGAG 1200 |
| Db | |
| 1460 | GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCAATTTAATAATAGTGTGAG 1519 |
| Qy | 1201 GTTATATATGCACAAAACACACACAGAAATATATTTCATGTCTATGTGTATATAGATCAAAT 1260 |
| Db | |
| 1520 | GTTATATATGCACAAAACACACACAGAAATATATTTCATGTCTATGTGTATATAGATCAAAT 1579 |
| Qy | 1261 GTTTTTTTTGGTATATATAACCAGGTACACCAGAGCTTACATATGTTTGAGTTAGACTCT 1320 |
| Db | |
| 1580 | GTTTTTTTTGGTATATATAACCAGGTACACCAGAGCTTACATATGTTTGAGTTAGACTCT 1639 |
| Qy | 1321 TAAAAATCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT 1380 |
| Db | |
| 1640 | TAAAAATCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT 1699 |
| Qy | 1381 AGGAGATAAAATTTATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGCTCTCTTA 1440 |
| Db | |
| 1700 | AGGAGATAAAATTTATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGCTCTCTTA 1759 |
| Qy | 1441 AAGAAAGCATCTTGATATATTAAAAATCAAAAGATGAGGCTTCTTACATATACATCTTAG 1500 |
| Db | |
| 1760 | AAGAAAGCATCTTGATATATTAAAAATCAAAAGATGAGGCTTCTTACATATACATCTTAG 1819 |
| Qy | 1501 TTGATTATTAAAAAGGAAAAAAGGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTTTC 1560 |
| Db | |
| 1820 | TTGATTATTAAAAAGGAAAAAAGGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTTTC 1879 |
| Qy | 1561 CATGAGAAGCACTGCATACCTTACCTATGTGAGACTGTAATAAACCTGTCTCCAAAAACCATGC 1620 |
| Db | |
| 1880 | CATGAGAAGCACTGCATACCTTACCTATGTGAGACTGTAATAAACCTGTCTCCAAAAACCATGC 1939 |
| Qy | 1621 CATAATAATATAAGTCTTTTAGAAATTAATATCATTTGTTTTTTTATGCAATTTTGTGAGG 1680 |
| Db | |
| 1940 | CATAATAATATAAGTCTTTTAGAAATTAATATCATTTGTTTTTTTATGCAATTTTGTGAGG 1999 |
| Qy | 1681 CATCCTTATTTCATTTAAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTTTATATATAGTC 1740 |
| Db | |
| 2000 | CATCCTTATTTCATTTAAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTTTATATATAGTC 2059 |
| Qy | 1741 CTACAAAAGACAAATGTATAAGCTGTAACAGAAATTTTGAATTTTCTTTTGCAAAACCC 1800 |
| Db | |
| 2060 | CTACAAAAGACAAATGTATAAGCTGTAACAGAAATTTTGAATTTTCTTTTGCAAAACCC 2119 |
| Qy | 1801 CTCCACAAAAGCAAAATCCTTTCAAGAATGGCATGGGCATTTCTGTATGAACCTTTTCCAGAT 1860 |
| Db | |
| 2120 | CTCCACAAAAGCAAAATCCTTTCAAGAATGGCATGGGCATTTCTGTATGAACCTTTTCCAGAT 2179 |
| Qy | 1861 GGTGTTTCAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAAACATCGAC 1920 |
| Db | |
| 2180 | GGTGTTCAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAAACATCGAC 2239 |
| Qy | 1921 GTAACTGGAAACCG 1934 |

Db 2240 GTAACCTGGAAACCG 2253
|||||
AAH46957
ID AAH46957 standard; cDNA; 4001 BP.
XX
AC AAH46957;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human secreted protein encoding cDNA (clone Id HE8TY90).
XX
KW Secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW nootropic; neuroprotective; antibacterial; virucide; fungicide; human;
KW ophthalmological; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200155430-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001431.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 12-SEP-2000; 2000US-0231968P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
PI Fiscella M, Ni J, Ruben SM, Barash SC;
XX
DR WPI; 2001-476220/51.
DR P-PSDB; AAB85547.
XX
17 isolated nucleic acid molecules encoding human secreted proteins, used
to preventing, treating or ameliorating a medical condition.
PS Claim 1; Page 430-432; 482pp; English.
XX
The invention provides novel human secreted proteins and polynucleotides
encoding them. The secreted proteins can be expressed by standard
recombinant methodology. The secreted proteins and polynucleotides are
used to prevent, treat or ameliorate a medical condition in e.g. humans,
mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can
also be used in diagnosing a pathological condition. The antibodies to
the proteins can also be used in alleviating symptoms associated with the
disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
linked immunosorbent assays (ELISA). Disorders which are diagnosed or
treated include autoimmune diseases e.g. rheumatoid arthritis,
hyperproliferative disorders e.g. neoplasms of the breast or liver,
cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
Alzheimer's disease, infections caused by bacteria, viruses and fungi and
ocular disorders e.g. corneal infection. The polypeptides can also be
used to aid wound healing and epithelial cell proliferation, to prevent
skin aging due to sunburn, to maintain organs before transplantation, for
supporting cell culture of primary tissues, to regenerate tissues and in
chemotaxis. The polypeptides can also be used as a food additive or
preservative to increase or decrease storage capabilities. The present
sequence represents a human secreted protein encoding cDNA
Sequence 4001 BP; 1218 A; 823 C; 796 G; 1156 T; 0 U; 8 Other;
Query Match 98.9%; Score 1913.6; DB 5; Length 4001;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1923; Conservative 7; Mismatches 1; Indels 3; Gaps 1;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGAAACGGCTACGTGCAGAGTCCTAGA 60
|||
Db 507 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGAAACGGCTACGTGCAGAGTCCTAGA 566
|||
QY 61 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 120
|||
Db 567 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 626
|||
QY 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC 180
|||
Db 627 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC 686
|||
QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAAGATATATCCGAAACCAGTACCATTATTAGAGGA 240
|||
Db 687 TGTAGGTATGATTTTGTGGAAGTTGAAAGATATATCCGAAACCAGTACCATTATTAGAGGA 746
|||
QY 241 CGATGGTGTGGACACAAGGAAGTTCTCCAGGATATAAATCAAGAACCAAAATTTAAA 300
|||
Db 747 CGATGGTGTGGACACAAGGAAGTTCTCCAGGATATAAATCAAGAACCAAAATTTAAA 806
|||
QY 301 ATCATTCAAGTCCGATGACTACTTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 360
|||
Db 807 ATCATTCAAGTCCGATGACTACTTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 866
|||
QY 361 TTGCTGGAAGATTTTCAACCCGCGCAGCAGCTTCAGAGACCACCTGGGAATCTGTCAACAGC 420
|||
Db 867 TTGCTGGAAGATTTTCAACCCGCGCAGCAGCTTCAGAGACCACCTGGGAATCTGTCAACAGC 926
|||
QY 421 TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
|||
Db 927 TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 986
|||
QY 481 GCTCTGGACAAAAAAATTCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 540
|||
Db 987 GCTCTGGACAAAAAAATTCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 1046
|||
QY 541 CCAGAGTCATGGCAAGAAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
|||
Db 1047 CCAGAGTCATGGCAAGAAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 1106
|||
QY 601 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGTCAATGATGATGCCAAG 660
|||
Db 1107 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGTCAATGATGATGCCAAG 1166
|||
QY 661 CGTTACAGTTGCACCTCCAGGAATTTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 720
|||
Db 1167 CGTTACAGTTGCACCTCCAGGAATTTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 1226
|||
QY 721 AATGTGCTCTTCTTTCCACGTTGCTCTCGTGCAGCGCTGTGGAGGAAATTTGTGGCTGT 780
|||
Db 1227 AATGTGCTCTTCTTTCCACGTTGCTCTCGTGCAGCGCTGTGGAGGAAATTTGTGGCTGT 1286
|||
QY 781 GGAACCTGCAACTGGAGTCTCTGCACATGCAATTCAGGGGAAAACCGTGAAAAGTATCAT 840
|||
Db 1287 GGAACCTGCAACTGGAGTCTCTGCACATGCAATTCAGGGGAAAACCGTGAAAAGTATCAT 1346
|||
QY 841 GAGGTATTACAGTTTGAGCCTTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 900
|||
Db 1347 GAGGTATTACAGTTTGAGCCTTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 1406
|||
QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATCGATTTGATCTGCAGCTCAAGACCA 960
|||
Db 1407 CTAGTTGACATCCAGTTGGATCACCATGAACGATGTGATTTGATCTGCAGCTCAAGACCA 1466
|||
QY 961 CCTCGATAAGAGAATGTGCACATCTTACATTAAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020
|||
Db 1467 CCTCGATAAGAGAATGTGCACATCTTACATTAAAGCCTGAAAGAACCTTTAGTTTAAGGA 1526
|||
QY 1021 GGGTGAGATAAGAGACCCCTTTTCTTACCAGCAACCAACTTACTACTAGCCTGCAATGCA 1080
|||
Db 1527 GGGTGAGATAAGAGACCCCTTTTCTTACCAGCAACCAACTTACTACTAGCCTGCAATGCA 1586
|||
QY 1081 ATGAACACAAGTGGTGGTCTGAGTCTCAGCCTTGCTTTGTTTAAATGCCATGGCAAGTAGAAA 1140
|||

|||||
1587 ATGAACACAAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1646
1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATGCAATTAATAATAGTGTGAG 1200
1647 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATGCAATTAATAATAGTGTGAG 1706
1201 GTTATATATGCACAAACACACACAGAAATATATTCTATGCTATGCTATATAGATCAAAAT 1260
1707 GTTATATATGCACAAACACACACAGAAATATATTCTATGCTATGCTATATAGATCAAAAT 1766
1261 GTTTTTTTTGGTATATATAACCAAGGTACACAGAGCTTACATATGTTTGGAGTTAGACTCT 1320
1767 GTTTTTTTTGGTATATATAACCAAGGTACACAGAGCTTACATATGTTTGGAGTTAGACTCT 1826
1321 TAAATCCTTTGCCAAATAAGGGATGGTCAAAATATATGAAACATGCTCTTTAGAAAATTT 1380
1827 TAAATCCTTTGCCAAATAAGGGATGGTCAAAATATATGAAACATGCTCTTTAGAAAATTT 1886
1381 AGGAGATAAATTTATTTTAAATTTTGAACACAAACAAATTTTGAATCTTGCTCTCTTA 1440
1887 AGGAGATAAATTTATTTTAAATTTTGAACACACRAAACAAATTTTGAATCTTGCTCTCTTA 1946
1441 AAGAAAGCATCTTGATATATTAATAAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG 1500
1947 AAGAAAGCATCTTGATATATTAATAAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG 2006
1501 TTGATTATTAAAAAGGAAAAA --GGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT 1557
2007 TTGATTATTAAAAAGGAAAAATATGGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT 2066
1558 TTCCATGAGAAAGCACTGCATACCTTACCTATGTGGACTGTAATAACCTGTCTCCAAAACCA 1617
2067 TTCCATGAGAAAGCACTGCATACCTTACCTATGTGGACTGTAATAACCTGTCTCCAAAACCA 2126
1618 TGCCATAATAATATAAGTGCTTTTAGAAATTAATCATTTGTTTATGCAATTTTGCTG 1677
2127 TGCCATAATAATATAAGTGCTTTTAGAAATTAATCATTTGTTTATGCAATTTTGCTG 2186
1678 AGGCATCCTTATTCATTTAAACACCTATCTCAAAAAAATTACTTAGAAGTTTTATTATA 1737
2187 AGGCATCCTTATTCATTTAAACACCTATCTCAAAAAAATTACTTAGAAGGKTTTATTATA 2246
1738 GTCCACAAAAGACAATGTATAAGCTGTAACAGAAATTTTGAATTTGTTTCTTTGCAAAA 1797
2247 GTCCACMAAAGACAATGTATAAGCTGTAACAGAAATTTTGAATTTGTTTCTTTGCAAAA 2306
1798 CCCCTCCACAAAAGCAAATCCTTTCAAGATGGCATGGGCATTTCTGTATGAACCTTTCCA 1857
2307 CCCCTCCACAAAAGCAAATCCTTTCAAGATGGCATGGGCATTTCTGTATGAACCTTTCCA 2366
1858 GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAAACATC 1917
2367 GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAAACATC 2426
1918 GACGTAACCTGGAAA 1931
2427 GACGTAACCTGGAAA 2440

RESULT 5
ABS58493
ID ABS58493 standard; cDNA; 4001 BP.
XX
AC ABS58493;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human secreted protein encoding cDNA #25.
XX

Human; secreted protein; autoimmune disease; blood coagulation disorder;
KW blood platelet disorder; hyperproliferative disorder; renal disorder; ss;
KW neurodegenerative disorder; cardiovascular disorder; vascular disorder;

KW respiratory disorder; endocrine disorder; reproductive disorder; gene;
KW gastrointestinal disorder; infectious disease; antianaemic; cytostatic;
KW antiarthritic; immunosuppressive; antiasthmatic; antidiabetic;
XX antiinflammatory; antipsoriatic; antiparkinsonian; neuroprotective.
OS Homo sapiens.
XX US2002120103-A1.
XX 29-AUG-2002.
XX 27-JUL-2001; 2001US-00915582.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 12-SEP-2000; 2000US-0231968P.
PR 17-JAN-2001; 2001WO-US001431.
XX (ROSE/) ROSEN C A.
PA (KOMA/) KOMATSOUIS G A.
PA (BAKE/) BAKER K P.
PA (BIRS/) BIRSE C E.
PA (SOPP/) SOPPET D R.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIP/) WEI P.
PA (EBNE/) EBNER R.
PA (DUAN/) DUAN D R.
PA (SHIY/) SHI Y.
PA (CHOI/) CHOI G H.
PA (FISC/) FISCELLA M.
PA (NIJJ/) NI J.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
PI Fiscella M, Ni J, Ruben SM, Barash SC;
XX WPI; 2002-608160/65.
DR P-PSDB; ABG76593.
DR
XX New secreted polypeptides and encoding polynucleotides, useful for
PT preventing, treating and diagnosing diseases e.g. anemia, cancer,
PT diabetes, asthma, psoriasis, Parkinson's and Alzheimer's.
XX
PS Claim 1; Page 373-375; 238pp; English.
XX The invention relates to an isolated nucleic acid molecule which encodes
CC a human secreted protein. The sequences are useful for diagnosing or
CC diagnosing a susceptibility to a pathological condition in a subject
CC comprising determining the presence or absence of a mutation in the DNA
CC or expression of the protein. The sequences are useful for identifying a
CC binding partner to the protein comprising contacting the protein with a
CC binding partner and determining whether the binding partner effects an
CC activity. The DNA and protein sequences are used for preventing, treating
CC or ameliorating a medical condition such as an autoimmune disease (e.g.
CC multiple sclerosis, myasthenia gravis), blood platelet disorders (e.g.
CC afibrinogenaemia, haemophilia), blood platelet disorders (e.g.
CC thrombocytopenia), hyperproliferative disorders (e.g. sarcooidosis, Sezary
CC syndrome), neurodegenerative disorders (e.g. Alzheimer's disease,
CC Parkinson's disease), renal disorders (e.g. renal vein thrombosis, kidney
CC infarction), cardiovascular disorders (e.g. cardiac arrest,
CC pericarditis), vascular disorders (e.g. aneurysm, ischaemia), respiratory
CC disorders (e.g. tonsillitis, laryngitis), endocrine disorders (e.g.
CC acromegaly, thyrotoxicosis), reproductive disorders (gonorrhea,
CC anorchia), gastrointestinal disorders (e.g. gastroenteritis, pyloric
CC stenosis), infectious diseases (e.g. polio, rubella) and cancer.
CC Sequences ABS58469-ABS58507 represent cDNA molecules encoding human
CC secreted proteins of the invention
XX
SQ Sequence 4001 BP; 1218 A; 823 C; 796 G; 1156 T; 0 U; 8 Other;

| | | | | | | | |
|-----------------------|------|--|------|--------------|---------------|------------|--------------|
| Query Match | | | | 98.9%; | Score 1913.6; | DB 6; | Length 4001; |
| Best Local Similarity | | | | 99.4%; | Pred. No. 0; | | |
| Matches 1923; | | | | Conservative | 7; | Mismatches | 1; |
| | | | | | | Indels | 3; |
| | | | | | | Gaps | 1; |
| QY | 1 | TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA | 60 | | | | |
| Db | 507 | TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA | 566 | | | | |
| QY | 61 | TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT | 120 | | | | |
| Db | 567 | TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT | 626 | | | | |
| QY | 121 | ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC | 180 | | | | |
| Db | 627 | ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC | 686 | | | | |
| QY | 181 | TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTTATTAGAGGA | 240 | | | | |
| Db | 687 | TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTTATTAGAGGA | 746 | | | | |
| QY | 241 | CGATGGTGTGGACACAAGGAAGTTCTCTCAAGGATAAAATCAAGAACGAACCAAATTTAAA | 300 | | | | |
| Db | 747 | CGATGGTGTGGACACAAGGAAGTTCTCTCAAGGATAAAATCAAGAACGAACCAAATTTAAA | 806 | | | | |
| QY | 301 | ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT | 360 | | | | |
| Db | 807 | ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT | 866 | | | | |
| QY | 361 | TTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC | 420 | | | | |
| Db | 867 | TTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC | 926 | | | | |
| QY | 421 | TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACCTCTGATTGGGAT | 480 | | | | |
| Db | 927 | TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACCTCTGATTGGGAT | 986 | | | | |
| QY | 481 | GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT | 540 | | | | |
| Db | 987 | GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT | 1046 | | | | |
| QY | 541 | CCAGAGTCATGGCAAGAAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC | 600 | | | | |
| Db | 1047 | CCAGAGTCATGGCAAGAAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC | 1106 | | | | |
| QY | 601 | AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG | 660 | | | | |
| Db | 1107 | AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG | 1166 | | | | |
| QY | 661 | CGTTACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC | 720 | | | | |
| Db | 1167 | CGTTACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC | 1226 | | | | |
| QY | 721 | AATGTGGTCTTCTTTCCAGTTGCTCCTCGTGCAGCGCTGTGGAGGAAATTTGTGGCTGT | 780 | | | | |
| Db | 1227 | AATGTGGTCTTCTTTCCAGTTGCTCCTCGTGCAGCGCTGTGGAGGAAATTTGTGGCTGT | 1286 | | | | |
| QY | 781 | GGAAGTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGGAAAAACCGTGAAAAAGTATCAT | 840 | | | | |
| Db | 1287 | GGAAGTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGGAAAAACCGTGAAAAAGTATCAT | 1346 | | | | |
| QY | 841 | GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT | 900 | | | | |
| Db | 1347 | GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT | 1406 | | | | |
| QY | 901 | CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA | 960 | | | | |
| Db | 1407 | CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA | 1466 | | | | |
| QY | 961 | CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA | 1020 | | | | |
| Db | 1467 | CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA | 1526 | | | | |
| QY | 1021 | GGGTGAGATAAGAGACCCCTTTTCTTACCAGCAACCAAACTTACTACTAGCTGCAATGCA | 1080 | | | | |

| | | | |
|----|------|--|------|
| Db | 1527 | GGGTGAGATAAGAGACCCCTTTTCCTACCCAGCAACCAAACTTACTACTAGCTGCAATGCA | 1586 |
| QY | 1081 | ATGAACACAAAGTGGTCTGAGTCTCAGCCCTTGTGTTAATGCCATGCCAAGTAGAAAA | 1140 |
| Db | 1587 | ATGAACACAAAGTGGTCTGAGTCTCAGCCCTTGTGTTAATGCCATGCCAAGTAGAAAA | 1646 |
| QY | 1141 | GGTATATCATCACTTCTATACCTAAAGAAATATATTCATGTCTATGTGTATATAGATCAAAT | 1200 |
| Db | 1647 | GGTATATCATCACTTCTATACCTAAAGAAATATATTCATGTCTATGTGTATATAGATCAAAT | 1706 |
| QY | 1201 | GTTATATATGCACAAAACACACACAGAAAATATATTCATGTCTATGTGTATATAGATCAAAT | 1260 |
| Db | 1707 | GTTATATATGCACAAAACACACACAGAAAATATATTCATGTCTATGTGTATATAGATCAAAT | 1766 |
| QY | 1261 | GTTTGTGTTGTTGTTATATTAACCAGGTACACCCAGAGCTTACATATGTTTGAGTTAGACTCT | 1320 |
| Db | 1767 | GTTTGTGTTGTTGTTATATTAACCAGGTACACCCAGAGCTTACATATGTTTGAGTTAGACTCT | 1826 |
| QY | 1321 | TAAAATCCTTTTGCACAAAATAAGGGATGGTCAAATATATGAAAACATGTCTTTAGAAAAATTT | 1380 |
| Db | 1827 | TAAAATCCTTTTGCACAAAATAAGGGATGGTCAAATATATGAAAACATGTCTTTAGAAAAATTT | 1886 |
| QY | 1381 | AGGAGATAAATTTATTTTAAATTTTGAACACAAAAAAATTTTGAATCTTGTCTCTCTTA | 1440 |
| Db | 1887 | AGGAGATAAATTTATTTTAAATTTTGAACACAAAAAAATTTTGAATCTTGTCTCTCTTA | 1946 |
| QY | 1441 | AAGAAAGCATCTTGTTATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG | 1500 |
| Db | 1947 | AAGAAAGCATCTTGTTATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG | 2006 |
| QY | 1501 | TTGATTTATTAATAAGGAAAAA ---GGTTTCAGAGAAAAAGGCCAATACCTAAGCATTTT | 1557 |
| Db | 2007 | TTGATTTATTAATAAGGAAAAAATATGGTTTCAGAGAAAAAGGCCAATACCTAAGCATTTT | 2056 |
| QY | 1558 | TTCCATGAGAAAGCACTGCATACCTTACCTATGTGGA CTGTAATAACCTGTCTCCAAAACCA | 1617 |
| Db | 2067 | TTCCATGAGAAAGCACTGCATACCTTACCTATGTGGACTRTAATAACCTGTCTCCAAAACCA | 2126 |
| QY | 1618 | TGCCATAATAATATAAGTGTCTTTAGAAATFAAATCATTTGTGTTTTTTATGCAATTTTGTG | 1677 |
| Db | 2127 | TGCCATAATAATATAAGTGTCTTTAGAAATFAAATCATTTGTGTTTTTTATGCAATTTTGTG | 2186 |
| QY | 1678 | AGGCATCCTTATTCATTTAACAACCTATCTCAAAAACTTACTTAGAAGGTTTTTTTATTATA | 1737 |
| Db | 2187 | AGGCATCCTTATTCATTTAACAACCTATCTCAAAAACTTACTTAGAAGGKTTTTTTATTATA | 2246 |
| QY | 1738 | GTCTACAAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTTCTTTTGCAAAA | 1797 |
| Db | 2247 | GTCTACMAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTTCTTTTGCAAAA | 2306 |
| QY | 1798 | CCCCTCCAAAAAGCAAAATCCTTTCAAGAATGGCATGGGCATCTGTATGAACCTTTTCCA | 1857 |
| Db | 2307 | CCCCTCCAAAAAGCAAAATCCTTTCAAGAATGGCATGGGCATCTGTATGAACCTTTTCCA | 2366 |
| QY | 1858 | GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAAACATTGAAACATC | 1917 |
| Db | 2367 | GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAMCATTTGAAACATC | 2426 |
| QY | 1918 | GACGTAACCTGGAAA 1931 | |
| Db | 2427 | GACGTAACCTGGAAA 2440 | |

RESULT 6
ADG65192
ID ADG65192 standard; DNA; 3739 BP.
XX
AC ADG65192;
XX
DT 11-MAR-2004 (first entry)
XX
DE Cell proliferation factor Fwa267 encoding sequence.

XX cell proliferation factor; Fwa267; cardiant; vasotropic;
KW angiocardioopathy; ds.
XX
OS Homo sapiens.
XX WO200268640-A1.
XX
PD 06-SEP-2002.
XX
PF 28-FEB-2002; 2002WO-CN000126.
XX
PR 28-FEB-2001; 2001CN-00109260.
XX (FUWA-) FU WAI HOSPITAL CHINESE ACAD MEDICAL SCI.
XX
PI Hui R, Chen J, Liu B, Liu Y;
XX WPI; 2003-058305/05.
DR P-PSDB; ADG65193.
DR
XX Human-originated cell proliferation factor Fwa267 polypeptide, and the
PT polypeptide encoding it, applicable in diagnosis and treatment of
PT angiocardioopathy.
XX
PS Claim 5; SEQ ID NO 1; 46pp; Chinese.
XX
CC The present invention relates to an isolated cell proliferation factor
CC Fwa267 polynucleotide which is cardiant and vasotropic in its action. The
CC polypeptide and its encoded polynucleotide are applicable in the
CC diagnosis and treatment of angiocardioopathy. The polypeptide is useful
CC for producing drug compositions for treating angiocardioopathy. The
CC present sequence represents the human cell proliferation factor Fwa267
CC encoding sequence.
XX
SQ Sequence 3739 BP; 1175 A; 732 C; 713 G; 1119 T; 0 U; 0 Other;

Query Match 98.9%; Score 1913.2; DB 10; Length 3739;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1928; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAAACGGCTACGTGCAGATCCTAGA 60
Db
251 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAAACGGCTACGTGCAGATCCTAGA 310
QY 61 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 120
Db 311 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 370
QY 121 ACACGGATACAGCTAGTGTGACAAATCAGTTGGATTAGAGGAAGCAGAAATGATATC 180
Db 371 ACACGGATACAGCTAGTGTGACAAATCAGTTGGATTAGAGGAAGCAGAAATGATATC 430
QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAACAGTACCATTATTAGAGGA 240
Db 431 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAACAGTACCATTATTAGAGGA 490
QY 241 CGATGGTGTGGACACAAGGAAGTTCTCCAGGATATAATCAAGAACGAAACCAAAATAAA 300
Db 491 CGATGGTGTGGACACAAGGAAGTTCTCCAGGATATAATCAAGAACGAAACCAAAATAAA 550
QY 301 ATCATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 360
Db 551 ATCATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 610
QY 361 TTGCTGGAAGATTCCAAACCCGACGAGCTTCAGAGACCAACTGGGAATCTGTCAACAGC 420
Db 611 TTGCTGGAAGATTCCAAACCCGACGAGCTTCAGAGACCAACTGGGAATCTGTCAACAGC 670
QY 421 TCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
Db 671 TCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 730

QY 481 GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540
Db 731 GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 790
QY 541 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 791 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 850
QY 601 AGGTCATACCATGACCCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 851 AGGTCATACCATGACCCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 910
QY 661 CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC 720
Db 911 CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC 970
QY 721 AATGTGGTCTCTTTCCACGTTGCCCTCCTCGTCGACGCGCTGTGAGGAAAATTTGTGGCTGT 780
Db 971 AATGTGGTCTCTTTCCACGTTGCCCTCCTCGTCGACGCGCTGTGAGGAAAATTTGTGGCTGT 1030
QY 781 GGAACCTGCAACTGGAGGTCCTGCACATGCAATTCAGGGAAAACCGTGAAAAAGTATCAT 840
Db 1031 GGAACCTGCAACTGGAGGTCCTGCACATGCAATTCAGGGAAAACCGTGAAAAAGTATCAT 1090
QY 841 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAAGACCATGGCT 900
Db 1091 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAAGACCATGGCT 1150
QY 901 CTAGTTGACATCCAGTTGGATCACATGAACGATCGGATTGTATCTGCAGCTCAAGACCA 960
Db 1151 CTAGTTGACATCCAGTTGGATCACATGAACGATGTGATTGTATCTGCAGCTCAAGACCA 1210
QY 961 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020
Db 1211 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1270
QY 1021 GGGTGAGATAAGAGACCCCTTTTCCACAGCAACCAACTTACTACTAGCCTGCAATGCA 1080
Db 1271 GGGTGAGATAAGAGACCCCTTTTCCACAGCAACCAACTTACTACTAGCCTGCAATGCA 1330
QY 1081 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1140
Db 1331 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1390
QY 1141 GGTATATCACTCAACTTCTATACCTAAGAAATATAGGATTGCATTTAATAATAGTTTGAG 1200
Db 1391 GGTATATCACTCAACTTCTATACCTAAGAAATATAGGATTGCATTTAATAATAGTTTGAG 1450
QY 1201 GTTATATATGCACAAAACACACACAGAAATATATTATGTCTATGTATATAGATCAAAAT 1260
Db 1451 GTTATATATGCACAAAACACACACAGAAATATATTATGTCTATGTATATAGATCAAAAT 1510
QY 1261 GTTTTTTTTTTGGTATATATAACCCAGGTACACCCAGAGCTTACATATGTTTGAGTTAGACTCT 1320
Db 1511 GTTTTTTTTTTGGTATATATAACCCAGGTACACCCAGAGCTTACATATGTTTGAGTTAGACTCT 1570
QY 1321 TAAATCCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAATTT 1380
Db 1571 TAAATCCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAATTT 1630
QY 1381 AGGAGATAAATTTATTTTAAATTTTGAACAACAATAATTTTGAATCTTGCTCTCTTA 1440
Db 1631 AGGAGATAAATTTATTTTAAATTTTGAACAACAATAATTTTGAATCTTGCTCTCTTA 1690
QY 1441 AAGAAAGCATCTTGATATATATAAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG 1500
Db 1691 AAGAAAGCATCTTGATATATATAAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG 1750
QY 1501 TTGATTATTAAAAAGGAAAAA -- -GGTTTCCAGAGAAAAGGCCAATACCTTAAGCATTTT 1557
Db 1751 TTGATTATTAAAAAGGAAAAAATATGGTTTCCAGAGAAAAGGCCAATACCTTAAGCATTTT 1810
QY 1558 TTCCATGAGAGCACTGCATACCTTACCTATGTGGACTGTATAACCTGTCTCCTCCAAAACCA 1617

Db 1811 TTCCATGAGAAGCACTGCATACCTTACCTATGTGGACTATAATAACCTGTCTCCAAAACCA 1870
Qy 1618 TGCCATAATAATAAGTGCCTTTAGAAATTAAATCATCTGTGTTTTTTATGCAATTTGCTG 1677
Db 1871 TGCCATAATAATAAGTGCCTTTAGAAATTAAATCATCTGTGTTTTTTATGCAATTTGCTG 1930
Qy 1678 AGGCATCCTTATTCAATTTAACACCTATCTCAAAAACCTTACTTAGAAGTTTTTTATTATA 1737
Db 1931 AGGCATGCTTATTCAATTTAACACCTATCTCAAAAACCTTACTTAGAAGTTTTTTATTATA 1990
Qy 1738 GTCCTACAAAAGACAATGTATAAGCTGTAAACAGAAATTTGAATTTGTTTTCTTTGCAAAA 1797
Db 1991 GTCCTACAAAAGACAATGTATAAGCTGTAAACAGAAATTTGAATTTGTTTTCTTTGCAAAA 2050
Qy 1798 CCCCTCCACAAAAGCAAAATCCTTTCAAGAATGGCATGGGCATTTCTGTATGAACCTTTCCA 1857
Db 2051 CCCCTCCACAAAAGCAAAATCCTTTCAAGAATGGCATGGGCATTTCTGTATGAACCTTTCCA 2110
Qy 1858 GATGTTGTTTCAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAAACATC 1917
Db 2111 GATGTTGTTTCAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAAACATC 2170
Qy 1918 GACGTAACCTGGAAA 1931
Db 2171 GACGTAACCTGGAAA 2184

RESULT 7
ADO20112
ID ADO20112 standard; cDNA; 3808 BP.
XX
AC ADO20112;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polynucleotide #511.
XX
KW Human; PRO; gene; ss; immune related disorder;
KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
KW juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
KW vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
KW renal disease; demyelinating disease; central nervous system;
KW peripheral nervous system; demyelinating polyneuropathy;
KW Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX
OS Homo sapiens.
XX
PN WO2004043361-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035268.
XX
PR 08-NOV-2002; 2002US-0425235P.
XX
PA (GETH) GENENTECH INC.
XX
PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX
DR WPI; 2004-420067/39.
DR P-PSDB; ADO20113.
XX
PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthropathy.
XX
PS Claim 1; SEQ ID NO 1076; 1731pp; English.
XX

CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polynucleotide of
CC the invention.
XX
SQ Sequence 3808 BP; 1191 A; 750 C; 738 G; 1129 T; 0 U; 0 Other;
Query Match 98.9%; Score 1913.2; DB 12; Length 3808;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1928; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACCGGTACGTGCAGAGTCTCTAGA 60
Db 320 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACCGGTACGTGCAGAGTCTCTAGA 379
QY 61 TTCCCGAACAGCTACCCAGGAACCTGCTCTCTGACATGGCGGCTTCACTCTCAGGAGAAT 120
Db 380 TTCCCGAACAGCTACCCAGGAACCTGCTCTCTGACATGGCGGCTTCACTCTCAGGAGAAT 439
QY 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180
Db 440 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 499
QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAGTACCATTTATTATTCT 240
Db 500 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAGTACCATTTATTATTAGGA 559
QY 241 CGATGGTGTGGACACAAAGGAAGTTCCTCAAGGATAAAAAATCAAGAACCAAAATTTAAA 300
Db 560 CGATGGTGTGGACACAAAGGAAGTTCCTCAAGGATAAAAAATCAAGAACCAAAATTTAAA 619
QY 301 ATCACAATTCAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 360
Db 620 ATCACAATTCAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 679
QY 361 TTGCTGGAAGATTTCCAAACCCGACGAGCTTCAGAGACCAACTGGAATCTGTCAACAGC 420
Db 680 TTGCTGGAAGATTTCCAAACCCGACGAGCTTCAGAGACCAACTGGAATCTGTCAACAGC 739
QY 421 TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
Db 740 TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 799
QY 481 GCTCTGGACAAAAAAATTCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540
Db 800 GCTCTGGACAAAAAAATTCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 859
QY 541 CCAGAGTCATGGCAAGAAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 860 CCAGAGTCATGGCAAGAAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC 919
QY 601 AGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 920 AGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 979
QY 661 CGTTACAGTTGCACCTCCAGGAATTTACTCGGTCAATATAAGAGAGAGAGCTGAAGTTGGCC 720
Db 980 CGTTACAGTTGCACCTCCAGGAATTTACTCGGTCAATATAAGAGAGAGAGCTGAAGTTGGCC 1039
QY 721 AATGTGGTCTTCTTTCCACGTTGCCCTCTCGTGACGGCTGTGGAGGAAATTTGGGCTGT 780
Db 1040 AATGTGGTCTTCTTTCCACGTTGCCCTCTCGTGACGGCTGTGGAGGAAATTTGGGCTGT 1099
QY 781 GGAACCTGTCAACTGGAGGTCTCTGCACATGCAATTCAGGGAAACCGTGAAAAAGTATCAT 840

Db 1100 GGAACGTGTCACCTGGAGGTCCTGCACATGCAATTCAGGGAACCGTGAAAAAGTATCAT 1159

QY 841 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900

Db 1160 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 1219

QY 901 CTAGTTGACATCCAGTTGGATCAACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 960

Db 1220 CTAGTTGACATCCAGTTGGATCAACCATGAACGATGTGATTGTATCTGCAGCTCAAGACCA 1279

QY 961 CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAAGGA 1020

Db 1280 CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAAGGA 1339

QY 1021 GGGTGAGATAAGAGACCCTTTTCCCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1080

Db 1340 GGGTGAGATAAGAGACCCTTTTCCCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1399

QY 1081 ATGAACACAAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1140

Db 1400 ATGAACACAAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1459

QY 1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTCGATTTAATAATAGTGTGAG 1200

Db 1460 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTCGATTTAATAATAGTGTGAG 1519

QY 1201 GTTATATATGCACAAAACACACACAGAAATATATTCATGTCTATGTGTATATAGATCAAAAT 1260

Db 1520 GTTATATATGCACAAAACACACACAGAAATATATTCATGTCTATGTGTATATAGATCAAAAT 1579

QY 1261 GTTTTTTTTGTGTATATATAACCAAGGTACACAGAGCTTACATATGTTGAGTTAGACTCT 1320

Db 1580 GTTTTTTTTGTGTATATATAACCAAGGTACACAGAGCTTACATATGTTGAGTTAGACTCT 1639

QY 1321 TAAATCCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCCTTTAGAAAATTT 1380

Db 1640 TAAATCCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCCTTTAGAAAATTT 1699

QY 1381 AGGAGATAAATTTATTTTAAATTTTGAACACAAAACAATTTTGAATCTTGCTCTCTTA 1440

Db 1700 AGGAGATAAATTTATTTTAAATTTTGAACACAAAACAATTTTGAATCTTGCTCTCTTA 1759

QY 1441 AAGAAAGCATCTGTATATTAAAAATCAAAGATGAGGCTTTCTTACATATACATCTTAG 1500

Db 1760 AAGAAAGCATCTGTATATTAAAAATCAAAGATGAGGCTTTCTTACATATACATCTTAG 1819

QY 1501 TTGATTATTAAAAAAGGAAAAA---GGTTTCCAGAGAAAAAGGCCAATACCTTAAGCATTTT 1557

Db 1820 TTGATTATTAAAAAAGGAAAAAATATGGTTTCCAGAGAAAAAGGCCAATACCTTAAGCATTTT 1879

QY 1558 TTCCATGAGAAGCACTGCATACCTTACCTATGTGGACTGTAATAACCTGTCTCCAAAACCA 1617

Db 1880 TTCCATGAGAAGCACTGCATACCTTACCTATGTGGACTAATAAACCTGTCTCCAAAACCA 1939

QY 1618 TGCCATAATAATATAAGTGCTTTAGAAAATTAATCATTTGTGTTTTTTATGCAATTTTGCTG 1677

Db 1940 TGCCATAATAATAAGTGCTTTAGAAAATTAATCATTTGTGTTTTTTATGCAATTTTGCTG 1999

QY 1678 AGGCATCCTTATTCATTTAAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTTATTATA 1737

Db 2000 AGGCATGCTTATTCATTTAAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTTATTATA 2059

QY 1738 GTCCTACAAAAGACAATGTATAAGCTGTAAACAAGATTTTGAATGTTTTTCTTTGCAAAA 1797

Db 2060 GTCCTACAAAAGACAATGTATAAGCTGTAAACAAGATTTTGAATGTTTTTCTTTGCAAAA 2119

QY 1798 CCCCTCCACAAAAGCAAAATCCTTTCAAGAATGCGATGGGCATTTCTGTATGAACCTTTCCA 1857

Db 2120 CCCCTCCACAAAAGCAAAATCCTTTCAAGAATGCGATGGGCATTTCTGTATGAACCTTTCCA 2179

QY 1858 GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACATC 1917

Db 2180 GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACATC 2239

QY 1918 GACGTAACCTGGAAA 1931

Db 2240 GACGTAACCTGGAAA 2253

RESULT 8
AAH46939

ID AAH46939 standard; cDNA; 3798 BP.

XX AAH46939;

DT 25-SEP-2001 (first entry)

XX Human secreted protein encoding cDNA (clone Id HGCNC48).

DE Secreted protein; immunosuppressive; antiarthritic; antirheumatic;
XX antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW nootropic; neuroprotective; antibacterial; virucide; fungicide; human;
KW opthalmological; gene therapy; ss.

OS Homo sapiens.

XX WO200155430-A1.

PN 02-AUG-2001.

PD 17-JAN-2001; 2001WO-US001431.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 12-SEP-2000; 2000US-0231968P.

XX (HUMA-) HUMAN GENOME.SCI INC.

PA Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;

XX Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;

PI Fiscella M, Ni J, Ruben SM, Barash SC;

XX WPI; 2001-476220/51.

DR P-PSDB; AAB85529.

XX Claim 1; Page 417-418; 482pp; English.

PT The invention provides novel human secreted proteins and polynucleotides
PT encoding them. The secreted proteins can be expressed by standard
PT recombinant methodology. The secreted proteins and polynucleotides are
PT used to prevent, treat or ameliorate a medical condition in e.g. humans,
PT mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can
PT also be used in diagnosing a pathological condition. The antibodies to
PT the proteins can also be used in alleviating symptoms associated with the
PT disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
PT linked immunosorbent assays (ELISA). Disorders which are diagnosed or
PT hyperproliferative disorders e.g. neoplasms of the breast or liver,
PT cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
PT e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
PT Alzheimer's disease, infections caused by bacteria, viruses and fungi and
PT ocular disorders e.g. corneal infection. The polypeptides can also be
PT used to aid wound healing and epithelial cell proliferation, to prevent
PT skin aging due to sunburn, to maintain organs before transplantation, for
PT supporting cell culture of primary tissues, to regenerate tissues and in
PT chemotaxis. The polypeptides can also be used as a food additive or
PT preservative to increase or decrease storage capabilities. The present
PT sequence represents a human secreted protein encoding cDNA

XX Sequence 3798 BP; 1189 A; 749 C; 737 G; 1123 T; 0 U; 0 Other;

Query Match 98.8%; Score 1911.6; DB 5; Length 3798;
Best Local Similarity 99.6%; Pred. No. 0;

| Matches 1927; Conservative 0; Mismatches 4; Indels 3; Gaps 1; | | | | |
|---|------|---|------|--|
| QY | 1 | TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTTAGA | 60 | |
| Db | 310 | TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTTAGA | 369 | |
| QY | 61 | TTCCCGAAGAGCTACCCAGGAACCTGCTCCTGACATGGCGGTTCACTCTCAGGAGAAAT | 120 | |
| Db | 370 | TTCCCGAAGAGCTACCCAGGAACCTGCTCCTGACATGGCGGTTCACTCTCAGGAGAAAT | 429 | |
| QY | 121 | ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGATTAGAGGAAGCAGAAAATGATATC | 180 | |
| Db | 430 | ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGATTAGAGGAAGCAGAAAATGATATC | 489 | |
| QY | 181 | TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTTATTAGAGGA | 240 | |
| Db | 490 | TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTTATTAGAGGA | 549 | |
| QY | 241 | CGATGGTGTGGACACAAGGAAGTTCCTCCAAGGATAAAATCAAGAACGAACCAAATTA | 300 | |
| Db | 550 | CGATGGTGTGGACACAAGGAAGTTCCTCCAAGGATAAAATCAAGAACGAACCAAATTA | 609 | |
| QY | 301 | ATCACAATCAAGTCCGATGACTCTTGTGGCTAAACCTGGATTCAAGATTTATTATCT | 360 | |
| Db | 610 | ATCACAATCAAGTCCGATGACTCTTGTGGCTAAACCTGGATTCAAGATTTATTATCT | 669 | |
| QY | 361 | TTGCTGGAAGATTTCCAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCACAAGC | 420 | |
| Db | 670 | TTGCTGGAAGATTTCCAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCACAAGC | 729 | |
| QY | 421 | TCTATTTCCAGGGGTATCCTATACTCTCCATCAGTAAACGGATCCCACTCTGATTGGGAT | 480 | |
| Db | 730 | TCTATTTCCAGGGGTATCCTATACTCTCCATCAGTAAACGGATCCCACTCTGATTGGGAT | 789 | |
| QY | 481 | GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT | 540 | |
| Db | 790 | GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT | 849 | |
| QY | 541 | CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC | 600 | |
| Db | 850 | CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC | 909 | |
| QY | 601 | AGGTCAATACCATGACCCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG | 660 | |
| Db | 910 | AGGTCAATACCATGACCCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG | 969 | |
| QY | 661 | CGTTACAGTTGCACTCCAGGAATTAATCTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC | 720 | |
| Db | 970 | CGTTACAGTTGCACTCCAGGAATTAATCTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC | 1029 | |
| QY | 721 | AATGGTCTTCTTTCCAGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTTGGGCTGT | 780 | |
| Db | 1030 | AATGGTCTTCTTTCCAGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTTGGGCTGT | 1089 | |
| QY | 781 | GGAATGTCAACTGGAGGTCCTGCACATGCAATTCAGGAAAAACCGTGAAAAAGTATCAT | 840 | |
| Db | 1090 | GGAATGTCAACTGGAGGTCCTGCACATGCAATTCAGGAAAAACCGTGAAAAAGTATCAT | 1149 | |
| QY | 841 | GAGGTATTACAGTTTGACCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT | 900 | |
| Db | 1150 | GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT | 1209 | |
| QY | 901 | CTAGTTGACATCCAGTTGGATCACCATGAACGATGGATTTGATCTGCGCTCAAGACCA | 960 | |
| Db | 1210 | CTAGTTGACATCCAGTTGGATCACCATGAACGATGGATTTGATCTGCGCTCAAGACCA | 1269 | |
| QY | 961 | CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCTGAAAGAACCTTTAGTTAAGGA | 1020 | |
| Db | 1270 | CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCTGAAAGAACCTTTAGTTAAGGA | 1329 | |
| QY | 1021 | GGTGAGATAAGAGACCCCTTTTCTTACCAGCAACCAAACTTACTAGCTGCAATGCA | 1080 | |
| Db | 1330 | GGTGAGATAAGAGACCCCTTTTCTTACCAGCAACCAAACTTACTAGCTGCAATGCA | 1389 | |

| | | | | |
|----|------|---|------|--|
| QY | 1081 | ATGAACACAAGTGGTTGCTGAGTCTCAGCCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA | 1140 | |
| Db | 1390 | ATGAACACAAGTGGTCTGCTGAGTCTCAGCCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA | 1449 | |
| QY | 1141 | GGTATATCATCAACTTCTATACCTTAAGAAATATAGGATTGCATTTAATAATAGTGTGAG | 1200 | |
| Db | 1450 | GGTATATCATCAACTTCTATACCTTAAGAAATATAGGATTGCATTTAATAATAGTGTGAG | 1509 | |
| QY | 1201 | GTTATATATGCACAAACACACACAGAAATATATTCATGTCTATGTGTATATAGATCAAAAT | 1260 | |
| Db | 1510 | GTTATATATGCACAAACACACACAGAAATATATTCATGTCTATGTGTATATAGATCAAAAT | 1569 | |
| QY | 1261 | GTTTTTTTTTGGTATATTAACCCAGGTACACACAGAGCTTACATATGTTTGAGTTAGACTCT | 1320 | |
| Db | 1570 | GTTTTTTTTTGGTATATTAACCCAGGTACACACAGAGCTTACATATGTTTGAGTTAGACTCT | 1629 | |
| QY | 1321 | TAAAATCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT | 1380 | |
| Db | 1630 | TAAAATCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT | 1689 | |
| QY | 1381 | AGGAGATAAAATTTATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGCTCTCTTA | 1440 | |
| Db | 1690 | AGGAGATAAAATTTATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGCTCTCTTA | 1749 | |
| QY | 1441 | AAGAAAGCATCTTGATATATTAATAATCAAAAGATGAGGCTTCTTACATATACATCTTAG | 1500 | |
| Db | 1750 | AAGAAAGCATCTTGATATATTAATAATCAAAAGATGAGGCTTCTTACATATACATCTTAG | 1809 | |
| QY | 1501 | TTGATTATTAAAAAAGGAAAAA ---GGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT | 1557 | |
| Db | 1810 | TTGATTATTAAAAAAGGAAAAAATATGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT | 1869 | |
| QY | 1558 | TTCCATGAGAAGCACTGCATACCTTACCCTATGTGGACTGTAAATACCTGTCTCCAAAAACCA | 1617 | |
| Db | 1870 | TTCCATGAGAAGCACTGCATACCTTACCCTATGTGGACTGTAAATACCTGTCTCCAAAAACCA | 1929 | |
| QY | 1618 | TGCCATAATAATAAAGTGCCTTTAGAAATTAATCATTTGTGTTTTTTATGCAATTTTGCTG | 1677 | |
| Db | 1930 | TGCCATAATAATAAAGTGCCTTTAGAAATTAATCATTTGTGTTTTTTATGCAATTTTGCTG | 1989 | |
| QY | 1678 | AGGCATCCTTTATTTAACAACCTATCTCAAAAACTTACTTAGAAGGTTTTTTTATTATA | 1737 | |
| Db | 1990 | AGGCATCCTTTATTTAACAACCTATCTCAAAAACTTACTTAGAAGGTTTTTTTATTATA | 2049 | |
| QY | 1738 | GTCTTACAAAAACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTTCTTTGCAAAA | 1797 | |
| Db | 2050 | GTCTTACAAAAACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTTCTTTGCAAAA | 2109 | |
| QY | 1798 | CCCCTCCAAAAAGCAAAATCCCTTCAAGAAATGGCATGGGCAATCTGTATGAACCTTTCCA | 1857 | |
| Db | 2110 | CCCCTCCAAAAAGCAAAATCCCTTCAAGAAATGGCATGGGCAATCTGTATGAACCTTTCCA | 2169 | |
| QY | 1858 | GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACATC | 1917 | |
| Db | 2170 | GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACATC | 2229 | |
| QY | 1918 | GACGTAACCTGGAAA 1931 | | |
| Db | 2230 | GACGTAACCTGGAAA 2243 | | |

| | |
|----------|--|
| RESULT 9 | |
| ABS58475 | |
| ID | ABS58475 standard; cDNA; 3798 BP. |
| XX | ABS58475; |
| AC | |
| XX | |
| DT | 05-NOV-2002 (first entry) |
| XX | Human secreted protein encoding cDNA #7. |
| DE | |
| XX | Human; secreted protein; autoimmune disease; blood coagulation disorder; |
| KW | |

KW blood platelet disorder; hyperproliferative disorder; renal disorder; ss;
KW neurodegenerative disorder; cardiovascular disorder; vascular disorder;
KW respiratory disorder; endocrine disorder; reproductive disorder; gene;
KW gastrointestinal disorder; infectious disease; antianaemic; cytostatic;
KW antiarthritic; immunosuppressive; antiasthmatic; antidiabetic;
KW antiinflammatory; antipsoriatic; antiparkinsonian; neuroprotective.

XX Homo sapiens.

OS US2002120103-A1.

XX 29-AUG-2002.

PF 27-JUL-2001; 2001US-00915582.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 12-SEP-2000; 2000US-0231968P.

PR 17-JAN-2001; 2001WO-US001431.

XX (ROSE/) ROSEN C A.

PA (KOMA/) KOMATSOU LIS G A.

PA (BAKE/) BAKER K P.

PA (BIRS/) BIRSE C E.

PA (SOPP/) SOPPET D R.

PA (OLSE/) OLSEN H S.

PA (MOOR/) MOORE P A.

PA (WEIP/) WEI P.

PA (EBNE/) EBNER R.

PA (DUAN/) DUAN D R.

PA (SHIY/) SHI Y.

PA (CHOI/) CHOI G H.

PA (FISC/) FISCELLA M.

PA (NIJJ/) NI J.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

XX

PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;

PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;

PI Fiscella M, Ni J, Ruben SM, Barash SC;

XX WPI; 2002-608160/65.

DR P-PSDB; ABG76575.

XX

PT New secreted polypeptides and encoding polynucleotides, useful for

PT preventing, treating and diagnosing diseases e.g. anemia, cancer,

PT diabetes, asthma, psoriasis, Parkinson's and Alzheimer's.

XX Claim 1; Page 357-359; 238pp; English.

XX

The invention relates to an isolated nucleic acid molecule which encodes a human secreted protein. The sequences are useful for diagnosing or diagnosing a susceptibility to a pathological condition in a subject comprising determining the presence or absence of a mutation in the DNA or expression of the protein. The sequences are useful for identifying a binding partner to the protein comprising contacting the protein with a binding partner and determining whether the binding partner effects an activity. The DNA and protein sequences are used for preventing, treating or ameliorating a medical condition such as an autoimmune disease (e.g. multiple sclerosis, myasthenia gravis), blood coagulation disorders (e.g. afibrinogenaemia, haemophilia), blood platelet disorders (e.g. thrombocytopenia), hyperproliferative disorders (e.g. sarcoidosis, Sezary syndrome), neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), renal disorders (e.g. renal vein thrombosis, kidney infarction), cardiovascular disorders (e.g. cardiac arrest, pericarditis), vascular disorders (e.g. aneurysm, ischaemia), respiratory disorders (e.g. tonsillitis, laryngitis), endocrine disorders (e.g. acromegaly, thyrotoxicosis), reproductive disorders (gonorrhea, anorchia), gastrointestinal disorders (e.g. gastroenteritis, pyloric stenosis), infectious diseases (e.g. polio, rubella) and cancer. Sequences ABS58469-ABS58507 represent cDNA molecules encoding human secreted proteins of the invention

| | | |
|----|----------------------------|--|
| SQ | Sequence | 3798 BP; 1189 A; 749 C; 737 G; 1123 T; 0 U; 0 Other; |
| | Query Match | 98.8%; Score 1911.6; DB 6; Length 3798; |
| | Best Local Similarity | 99.6%; Pred. No. 0; |
| | Matches 1927; Conservative | 0; Mismatches 4; Indels 3; Gaps 1; |
| QY | 1 | TTGTACCGAAGAGATGAGACCATCCAGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 60 |
| | | |
| Db | 310 | TTGTACCGAAGAGATGAGACCATCCAGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 369 |
| | | |
| QY | 61 | TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 120 |
| | | |
| Db | 370 | TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 429 |
| | | |
| QY | 121 | ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180 |
| | | |
| Db | 430 | ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 489 |
| | | |
| QY | 181 | TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGA 240 |
| | | |
| Db | 490 | TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGA 549 |
| | | |
| QY | 241 | CGATGCTGTGGACACAAGGAAGTTCTCTCCAAGGATAAAAAATCAAGAACGAACCAATATAA 300 |
| | | |
| Db | 550 | CGATGCTGTGGACACAAGGAAGTTCTCTCCAAGGATAAAAAATCAAGAACGAACCAATATAA 609 |
| | | |
| QY | 301 | ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 360 |
| | | |
| Db | 610 | ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 669 |
| | | |
| QY | 361 | TTGCTGGAAGATTTCCAACCCGCGCAGCAGTTTCAAGAGACCAACTGGGAATCTGTCAACAAGC 420 |
| | | |
| Db | 670 | TTGCTGGAAGATTTCCAACCCGCGCAGCAGTTTCAAGAGACCAACTGGGAATCTGTCAACAAGC 729 |
| | | |
| QY | 421 | TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACCTCGATTGCGGAT 480 |
| | | |
| Db | 730 | TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACCTCGATTGCGGAT 789 |
| | | |
| QY | 481 | GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540 |
| | | |
| Db | 790 | GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 849 |
| | | |
| QY | 541 | CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600 |
| | | |
| Db | 850 | CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 909 |
| | | |
| QY | 601 | AGGTCATACCATGACCCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660 |
| | | |
| Db | 910 | AGGTCATACCATGACCCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 969 |
| | | |
| QY | 661 | CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAGAGAGTGAAGTTGGCC 720 |
| | | |
| Db | 970 | CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAGAGAGTGAAGTTGGCC 1029 |
| | | |
| QY | 721 | AATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGACGCGCTGTGGAGGAAATTTGTGGCTGT 780 |
| | | |
| Db | 1030 | AATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGACGCGCTGTGGAGGAAATTTGTGGCTGT 1089 |
| | | |
| QY | 781 | GGAACCTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 840 |
| | | |
| Db | 1090 | GGAACCTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 1149 |
| | | |
| QY | 841 | GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900 |
| | | |
| Db | 1150 | GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 1209 |
| | | |
| QY | 901 | CTAGTTGACATCCAGTTGGATCACCATGAACGATCGGATTGTATCTGAGCTCAAGACCA 960 |
| | | |
| Db | 1210 | CTAGTTGACATCCAGTTGGATCACCATGAACGATGTGATTGTATCTGAGCTCAAGACCA 1269 |
| | | |
| QY | 961 | CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTTAGTTTAAGGA 1020 |
| | | |
| Db | 1270 | CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTTAGTTTAAGGA 1329 |
| | | |

QY 121 ACACGGATACAGCTAGTGTGTTTGACAATCAAGTTGGATTAGAGGAAGCAGAAAAATGATATC 180
Db 360 ACACGGATACAGCTAGTGTGTTTGACAATCAAGTTGGATTAGAGGAAGCAGAAAAATGATATC 419
QY 181 TGAGGTATGATTTGTGGAAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGA 240
Db 420 TGAGGTATGATTTGTGGAAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGA 479
QY 241 CGATGGTGTGGACACAAGGAAGTTCCCTCCAAGGATAAAAATCAAGAACGAAACCAAAATTAAA 300
Db 480 CGATGGTGTGGACACAAGGAAGTTCCCTCCAAGGATAAAAATCAAGAACGAAACCAAAATTAAA 539
QY 301 ATCACATTCAAGTCCGATGACTACTTTGTGCTTAAACCTGGATTCAAGATTATTATTCT 360
Db 540 ATCACATTCAAGTCCGATGACTACTTTGTGCTTAAACCTGGATTCAAGATTATTATTCT 599
QY 361 TTGCTGGAAGATTTCACACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCACAAGC 420
Db 600 TTGCTGGAAGATTTCACACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCACAAGC 659
QY 421 TCTATTTACGGGTATCCTATAAATCTCTCAATCAGTAACGGATCCCACTCTGATTGCGGAT 480
Db 660 TCTATTTACGGGTATCCTATAAATCTCTCAATCAGTAACGGATCCCACTCTGATTGCGGAT 719
QY 481 GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 540
Db 720 GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 779
QY 541 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 780 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 839
QY 601 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 840 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 899
QY 661 CGTTACAGTTGCACTCCAGGAATTAATCTCGTCAATATAAGAGAAGAGCTGAAGTTGGCC 720
Db 900 CGTTACAGTTGCACTCCAGGAATTAATCTCGTCAATATAAGAGAAGAGCTGAAGTTGGCC 959
QY 721 AATGTGCTCTCTTCCACGTTGCCCTCCTCGTGCAGCGCTGTGGAGGAATTTGGCTGT 780
Db 960 AATGTGCTCTCTTCCACGTTGCCCTCCTCGTGCAGCGCTGTGGAGGAATTTGGCTGT 1019
QY 781 GGAAGTGTCAACTGAGGCTCCTGCACATGCAATTCAGGGAACCCGTGAAAAAGTATCAT 840
Db 1020 GGAAGTGTCAACTGAGGCTCCTGCACATGCAATTCAGGGAACCCGTGAAAAAGTATCAT 1079
QY 841 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTTAAGACCATGGCT 900
Db 1080 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTTAAGACCATGGCT 1139
QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAAGCTCAAGACCA 960
Db 1140 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAAGCTCAAGACCA 1199
QY 961 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020
Db 1200 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1259
QY 1021 GGGTGAGATAAGAGACCCCTTTTCCCTACCAGCAACCAAACTTACTAGCTGCAATGCA 1080
Db 1260 GGGTGAGATAAGAGACCCCTTTTCCCTACCAGCAACCAAACTTACTAGCTGCAATGCA 1319
QY 1081 ATGAACACAAAGTGTGCTGAGTCTCAGCCCTTGTGTTTAATGCCATGCCAAGTAGAAA 1140
Db 1320 ATGAACACAAAGTGTGCTGAGTCTCAGCCCTTGTGTTTAATGCCATGCCAAGTAGAAA 1379
QY 1141 GGTATATCATCAACTTCTATATACCTAAGAAATATAGGATTGCATTTAATATAGTGTGAG 1200
Db 1380 GGTATATCATCAACTTCTATATACCTAAGAAATATAGGATTGCATTTAATATAGTGTGAG 1439

QY 1201 GTTATATATGCACAAAACACACACAGAAATATATTCTATGTCTATATATAGATCAAAT 1260
Db 1440 GTTATATATGCACAAAACACACACAGAAATATATTCTATGTCTATGTCTATATAGATCAAAT 1499
QY 1261 GTTTTTTTTGGTATATATAACCAGGTACACAGAGCTTACATATGTTTGAGTTAGACTCT 1320
Db 1500 GTTTTTTTTGGTATATATAACCAGGTACACAGAGCTTACATATGTTTGAGTTAGACTCT 1559
QY 1321 TAAAAATCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT 1380
Db 1560 TAAAAATCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT 1619
QY 1381 AGGAGATAAAATTTATTTTAAATTTTGAAACACAAAAACAATTTTGAAATCTTCTCTTATA 1440
Db 1620 AGGAGATAAAATTTATTTTAAATTTTGAAACACAAAAACAATTTTGAAATCTTCTCTTATA 1679
QY 1441 AAGAAAGCATCTTGATATATTAAAAATCAAAAAGATGAGGCTTTCTTACATATACATCTTAG 1500
Db 1680 AAGAAAGCATCTTGATATATTAAAAATCAAAAAGATGAGGCTTTCTTACATATACATCTTAG 1739
QY 1501 TTGATTATTAAAAAAGGAAAAA---GGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT 1557
Db 1740 TTGATTATTAAAAAAGGAAAAAATATGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT 1799
QY 1558 TTCCATGAGAAGCACTGCATACCTTACCTATGTGGACTGTAATAACCTGTCTCCAAAAACCA 1617
Db 1800 TTCCATGAGAAGCACTGCATACCTTACCTATGTGGACTATAATAACCTGTCTCCAAAAACCA 1859
QY 1618 TGCCATAATAATATAAGTGCTTTTAGAAATTAATCATTTGTTTTTTTATGCAATTTTGCTG 1677
Db 1860 TGCCATAATAATATAAGTGCTTTTAGAAATTAATCATTTGTTTTTTTATGCAATTTTGCTG 1919
QY 1678 AGGCATCCTTATTCAATTTAACACCTATCTCAAAAACTTACTTAGAAGTTTTTATTATA 1737
Db 1920 AGGCATCCTTATTCAATTTAACACCTATCTCAAAAACTTACTTAGAAGTTTTTATTATA 1979
QY 1738 GTCCTACAAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTTCTTTGCAAAA 1797
Db 1980 GTCCTACAAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTTCTTTGCAAAA 2039
QY 1798 CCCCTCCACAAAAAGCAAAATCCCTTTCAAGAAATGGCATGGGCATTTCTGTATGAACCTTTCCA 1857
Db 2040 CCCCTCCACAAAAAGCAAAATCCCTTTCAAGAAATGGCATGGGCATTTCTGTATGAACCTTTCCA 2099
QY 1858 GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAAACATTGAAACATC 1917
Db 2100 GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAAACATTGAAACATC 2159
QY 1918 GACGTAACTGGAAA 1931
Db 2160 GACGGTAACTGGAA 2173

RESULT 11

AAD25488
ID AAD25488 standard; DNA; 3736 BP.

XX AAD25488;

XX 26-MAR-2002 (first entry)

XX Human LP85 DNA #1.

DE LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulneryary;
XX osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder;
KW MSD; therapy; bone growth; cartilage differentiation; wound healing;
KW neuron growth; bone fracture; osteoporosis; osteopenia; arthritis;
KW sarcopenia; periodontal disease; tissue atrophy; endocrine disorder;
KW muscle loss; immobility; bone density; ds.

OS Homo sapiens.

XX XX

Location/Qualifiers

Key

FH

```
FT CDS 114..1226
FT /*tag= a
FT /product= "Human LP85 protein"
FT sig_peptide 114..149
FT /*tag= b
FT mat_peptide 150..1223
FT /*tag= c
FT /product= "Human mature LP85 protein"
XX
PN W0200189450-A2.
XX
PD 29-NOV-2001.
XX
PF 08-MAY-2001; 2001WO-US011755.
XX
PR 19-MAY-2000; 2000US-0205424P.
PR 11-JAN-2001; 2001US-0261071P.
PR 11-JAN-2001; 2001US-0261076P.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;
PI Witcher DR, Wroblewski VJ;
XX
DR WPI; 2002-083040/l1.
DR P-PSDB; AAE15819.
XX
PT Analog of a platelet-derived growth factor homolog, LP85 useful for
PT treating osteoporosis, arthritis, sarcopenia, wounds, has one or more
PT amino acid substitutions which destroy the tripeptidyl sequence of native
PT LP85.
XX
PS Disclosure; Page 106-109; 117pp; English.
XX
CC The present invention relates to LP85, an analogue of platelet-derived
CC growth factor (PDGF) homologue. Sequences of the invention are useful for
CC the manufacture of a medicament for treating musculoskeletal disorder
CC (MSD) which include promoting bone growth, cartilage differentiation and
CC function, wound healing, neuron growth, preventing cartilage degradation
CC or neuronal degeneration. They are useful for treating bone fractures,
CC osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease,
CC tissue atrophy, traumatised connective tissues, grafted connective
CC tissues and/or transplanted organs, bone or muscle loss due to
CC malignancy, endocrine disorders and immobility. They are also used for
CC prophylactically increasing or maintaining bone density in a mammal. The
CC present sequence is a DNA encoding human LP85 protein
XX
SQ Sequence 3736 BP; 1164 A; 736 C; 718 G; 1118 T; 0 U; 0 Other;
Query Match 98.4%; Score 1903.6; DB 6; Length 3736;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1922; Conservative 0; Mismatches 9; Indels 3; Gaps 1;
QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 60
Db |||||
Db 258 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 317
QY 61 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACCTCAGGAGAAT 120
Db |||||
Db 318 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACCTCAGGAGAAT 377
QY 121 ACACGGATACAGCTAGTGTGTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC 180
Db |||||
Db 378 ACACGGATACAGCTAGTGTGTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC 437
QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 240
Db |||||
Db 438 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 497
QY 241 CGATGGTGTGGACACAAAGGAAGTTCTCCAAGGATAAAATCAAGAACGAAACCAAAATTAA 300
Db |||||
Db 498 CGATGGTGTGGACACAAAGGAAGTTCTCCAAGGATAAAATCAAGAACGAAACCAAAATTAA 557
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QY 301 ATCACATTCAAGTCOGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 360
Db |||||
Db 558 ATCACATTCAAGTCOGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 617
QY 361 TTGCTGGAAGATTTCCAAACCCGCGCAGCGCTTCAGAGACCAACTGGGAATCTGTCAACAGC 420
Db |||||
Db 618 TTGCTGGAAGATTTCCAAACCCGCGCAGCGCTTCAGAGACCAACTGGGAATCTGTCAACAGC 677
QY 421 TCTATTTTCAGGGGTATCCTATAAATCTCCATCAGTAACGGATCCCACCTCTGATTGCGGAT 480
Db |||||
Db 678 TCTATTTTCAGGGGTATCCTATAAATCTCCATCAGTAACGGATCCCACCTCTGATTGCGGAT 737
QY 481 GCTCTGGACAAAATAATTGCAGAAATTTGTATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 540
Db |||||
Db 738 GCTCTGGACAAAATAATTGCAGAAATTTGTATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 797
QY 541 CCAGAGTCATGGCAAGAAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db |||||
Db 798 CCAGAGTCATGGCAAGAAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 857
QY 601 AGGTATACCATGACCGGAAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db |||||
Db 858 AGGTATACCATGACCGGAAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 917
QY 661 CGTTACAGTTGCACTCCAGGAATTTACTCGGTCAATATAAGAGAGAGAGTGAAGTTGGCC 720
Db |||||
Db 918 CGTTACAGTTGCACTCCAGGAATTTACTCGGTCAATATAAGAGAGAGAGTGAAGTTGGCC 977
QY 721 AATGTGGTCTTCTTTCCACGTTGCCCTCCTCGTGCAGCGCTGTGGAGGAAATTTGGCTGT 780
Db |||||
Db 978 AATGTGGTCTTCTTTCCACGTTGCCCTCCTCGTGCAGCGCTGTGGAGGAAATTTGGCTGT 1037
QY 781 GGAACCTGTCAACTGGAGGTCCTGTCACATGCAATTCAGGGGAAACCCGTGAAAAAGTATCAT 840
Db |||||
Db 1038 GGAACCTGTCAACTGGAGGTCCTGTCACATGCAATTCAGGGGAAACCCGTGAAAAAGTATCAT 1097
QY 841 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGAGGAGGGGTAGAGCTAAGACCATGGCT 900
Db |||||
Db 1098 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGAGGAGGGGTAGAGCTAAGACCATGGCT 1157
QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 960
Db |||||
Db 1158 CTAGTTGACATCCAGTTGGATCACCATGAACGATGTTGATTGTATCTGCAGCTCAAGACCA 1217
QY 961 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCCTGAAAGAACCTTTAGTTTAAGGA 1020
Db |||||
Db 1218 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCCTGAAAGAACCTTTAGTTTAAGGA 1277
QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1080
Db |||||
Db 1278 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1337
QY 1081 ATGAAACACAAGTGGTTGCTGAGTCTCAGCCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1140
Db |||||
Db 1338 ATGAAACACAAGTGGTTGCTGAGTCTCAGCCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1397
QY 1141 GGTATATCATCAACTTCTATACCTTAAGAATATAGGATTGCATTTAATAATAGTGTGAG 1200
Db |||||
Db 1398 GGTATATCATCAACTTCTATACCTTAAGAATATAGGATTGCATTTAATAATAGTGTGAG 1457
QY 1201 GTTATATATGCACAAACACACACAGAAATATATTCAATGTCATGTGTATATAGATCAAAAT 1260
Db |||||
Db 1458 GTTATATATGCACAAACACACACAGAAATATATTCAATGTCATGTGTATATAGATCAAAAT 1517
QY 1261 GTTTTTTTTGGTATATATAACAGGTACACAGAGCTTACATATGTTTGGATTAGACTCT 1320
Db |||||
Db 1518 GTTTTTTTTGGTATATATAACAGGTACACAGAGCTTACATATGTTTGGATTAGACTCT 1577
QY 1321 TAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT 1380
Db |||||
Db 1578 TAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT 1637
QY 1381 AGGAGATAAAATTTATTTTAAATTTTGAAACACAAACAAATTTTGAATCTTGCCTCTTA 1440
```

||||| 1638 AGGAGATAAATTTATTTTAAATTTTGAAACACAAAACAATTTTGAATCTTGCTCTTA 1697
Db
||||| 1441 AAGAAAGCATCTTGATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG 1500
QY
||||| 1698 AAGAAAGCATCTTGATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG 1757
Db
||||| 1501 TTGATTATTAATAAGGAAAAA---GGTTTCCAGAGAAAAAGGCCAATACCTAAAGCATTTT 1557
QY
||||| 1758 TTGATTATTAATAAGGAAAAAATATGGTTTCCAGAGAAAAAGGCCAATACCTAAAGCATTTT 1817
Db
||||| 1558 TTCCATGAGAGCACTGCATACCTTACCTATGTGGACTGTAATAACCTGTCTCCAAAACCA 1617
QY
||||| 1818 TTCCATGAGAGCACTGCATACCTTACCTATGTGGACTATAATAACCTGTCTCCAAAACCA 1877
Db
||||| 1618 TGCCATAATAATAAGTGCTTTTAGAATTAATCAATTTGTGTTTTTATGCAATTTTGCTG 1677
QY
||||| 1878 TGCCATAATAATAAGTGCTTTTAGAATTAATCAATTTGTGTTTTTATGCAATTTTGCTG 1937
Db
||||| 1678 AGGCATCTTATTCATTTAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTTATTATA 1737
QY
||||| 1938 AGGCATCTTATTCATTTAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTTATTATA 1997
Db
||||| 1738 GTCTACAAAAGACAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTTCTTTGCAAAA 1797
QY
||||| 1998 GTCTACAAAAGACAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTTCTTTGCAAAA 2057
Db
||||| 1798 CCCCTCCAAAAAGCAAATCCTTTCAAGAATGGCATGGGCATTTCTGTATGAACCTTTCCA 1857
QY
||||| 2058 CCCCTCCAAAAAGCAAATCCTTTCAAGAATGGCATGGGCATTTCTGTATGAACCTTTCCA 2117
Db
||||| 1858 GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAAGTGAACATTGAAACATC 1917
QY
||||| 2118 GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAAGTGAACATTGAAACATC 2177
Db
||||| 1918 GACGTAACTGGAAA 1931
QY
||||| 2178 GACGGTAACTGGAA 2191
Db

RESULT 12
AAF24196
ID AAF24196 standard; DNA; 3853 BP.
XX
AC AAF24196;
XX
DT 02-APR-2001 (first entry)
XX
DE Human VEGF-G cDNA.
XX
KW Vascular endothelial growth factor; VEGF; cancer; cell; angiogenesis; ss.
XX
OS Homo sapiens.
XX
PN WO200100878-A2.
XX
PD 04-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-US018085.
XX
PR 30-JUN-1999; 99US-00343671.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gearing DP;
XX
DR WPI; 2001-050129/06.
XX
PT New vascular endothelial growth factor family member used for diagnosis
PT and treatment of deregulated cell growth e.g. cancer, disorders involving
PT aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases.
XX
PS Claim 1; Fig 1; 142pp; English.

XX The present invention relates to a vascular endothelial growth factor
CC (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid molecules
CC are used as modulating agents or as targets for developing modulating
CC agents to regulate a variety of cellular processes e.g. cell
CC proliferation, differentiation, migration and wound repair. VEGF-G
CC modulators, i.e. VEGF-G protein, peptide, peptidomimetic or nucleic acid
CC are used to treat a subject with aberrant VEGF-G protein or nucleic acid
CC expression or activity e.g. deregulated cell growth, such as cancer,
CC hyperproliferative bone disorders, disorders involving aberrant angiogenesis
CC e.g. psoriasis, and chronic inflammatory diseases e.g. rheumatoid
CC arthritis. VEGF-G gene expression is inhibited through the administration
CC of antisense molecules or ribozymes and by targeting the regulatory
CC region of VEGF-G to prevent transcription of the gene in target cells
XX
SQ Sequence 3853 BP; 1194 A; 771 C; 757 G; 1131 T; 0 U; 0 Other;

Query Match 98.4%; Score 1902.8; DB 4; Length 3853;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1929; Conservative 0; Mismatches 2; Indels 5; Gaps 2;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGAGAGTCTCTAGA 60
Db
357 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGAGAGTCTCTAGA 416
QY 61 TTCCCGAACAGCTACCCAGGAACCTGCTCTGACATGGCGGCTTCACTCTCAGGAGAAT 120
Db 417 TTCCCGAACAGCTACCCAGGAACCTGCTCTGACATGGCGGCTTCACTCTCAGGAGAAT 476
QY 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180
Db 477 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 536
QY 181 TGTTAGTATGATTTTGTGGAAGTTGAAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 240
Db 537 TGTTAGTATGATTTTGTGGAAGTTGAAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 596
QY 241 CGATGTTGGAACAACAAGGAAGTTCTCCAGGATATAAATCAAGAACCAAAATTTAAA 300
Db 597 CGATGTTGGAACAACAAGGAAGTTCTCCAGGATATAAATCAAGAACCAAAATTTAAA 656
QY 301 ATCACAATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 360
Db 657 ATCACAATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 716
QY 361 TTGCTGGAAGATTTCCAAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCACAAGC 420
Db 717 TTGCTGGAAGATTTCCAAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCACAAGC 776
QY 421 TCTATTTCAGGGGTATCCTATTAACCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
Db 777 TCTATTTCAGGGGTATCCTATTAACCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 836
QY 481 GCTCTGGACAAAAAAATTCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540
Db 837 GCTCTGGACAAAAAAATTCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 896
QY 541 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 897 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 956
QY 601 AGGTCATACCATGACCCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGCCAAG 660
Db 957 AGGTCATACCATGACCCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGCCAAG 1016
QY 661 CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAGAGAGCTGAAGTTGGCC 720
Db 1017 CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAGAGAGCTGAAGTTGGCC 1076
QY 721 AATGTGGTCTTCTTTCCACGTTGCTCTGTCAGCGCTGTGGAGGAAATTTGTGGCTGT 780
Db 1077 AATGTGGTCTTCTTTCCACGTTGCTCTGTCAGCGCTGTGGAGGAAATTTGTGGCTGT 1136

QY 781 GGAACGTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAACCGTGAAAAAGTATCAT 840
Db |||||||
1137 GGAACGTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAACCGTGAAAAAGTATCAT 1196
QY 841 GAGGTATTACAGTTTGAGCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 900
Db |||||||
1197 GAGGTATTACAGTTTGAGCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 1256
QY 901 CTAGTTGACATCCAGTTGATCACCATGACATGCGATGCGATGTATCTGCAGCTCAAGACCA 960
Db |||||||
1257 CTAGTTGACATCCAGTTGATCACCATGACATGCGATGTATCTGCAGCTCAAGACCA 1316
QY 961 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTAAAGGA 1020
Db |||||||
1317 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTAAAGGA 1376
QY 1021 GGGTGAGATAAGAGACCCCTTTTCTTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1080
Db |||||||
1377 GGGTGAGATAAGAGACCCCTTTTCTTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1436
QY 1081 ATGAACACAAAGTGGTTGCTGAGTCTCAGCCCTTGCTTTGTTAAATGCCATGGCAAGTAGAAA 1140
Db |||||||
1437 ATGAACACAAAGTGGTTGCTGAGTCTCAGCCCTTGCTTTGTTAAATGCCATGGCAAGTAGAAA 1496
QY 1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATGCAATTAATAATAGTGTGAG 1200
Db |||||||
1497 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATGCAATTAATAATAGTGTGAG 1556
QY 1201 GTTATATATGCACAAACACACACAGAAATATATTATGTCATGTATGTATATAGATCAAAT 1260
Db |||||||
1557 GTTATATATGCACAAACACACACAGAAATATATTATGTCATGTATGTATATAGATCAAAT 1616
QY 1261 G- -TTTTTTTTTGGTATATATAAACAGGTACACCCAGGCTTACATATGTTTGAGTTAGACT 1318
Db |||||||
1617 GTTTTTTTTTTGGTATATATAAACAGGTACACCCAGGTTACATATGTTTGAGTTAGACT 1676
QY 1319 CTTAAAAATCCTTTGCCAAAATAAGGGATGGTCAATATATGAAACATGTCTTTAGAAAAT 1378
Db |||||||
1677 CTTAAAAATCCTTTGCCAAAATAAGGGATGGTCAATATATGAAACATGTCTTTAGAAAAT 1736
QY 1379 TTAGGAGATAAAATTTTAAATTTTGAAACACAAAACAATTTTGAAATCTTGCTCTCT 1438
Db |||||||
1737 TTAGGAGATAAAATTTTAAATTTTGAAACACGAAACAATTTTGAAATCTTGCTCTCT 1796
QY 1439 TAAAGAAAGCATCTTGATATATTAATAAAATCAAAGATGAGGCTTTCTTACATATACATCTT 1498
Db |||||||
1797 TAAAGAAAGCATCTTGATATATTAATAAAATCAAAGATGAGGCTTTCTTACATATACATCTT 1856
QY 1499 AGTTGATTATTAATAAAAGGAAAAA- -GGTTTCCAGAGAAAAAGGCCAATACCTAAGCATT 1555
Db |||||||
1857 AGTTGATTATTAATAAAAGGAAAAAATATGGTTTCCAGAGAAAAAGGCCAATACCTAAGCATT 1916
QY 1556 TTTTCCATGAGAAGCACTGCATACTTACCTATGFGACTGTAATAACCTGTCTCCAAAAC 1615
Db |||||||
1917 TTTTCCATGAGAAGCACTGCATACTTACCTATGFGACTGTAATAACCTGTCTCCAAAAC 1976
QY 1616 CATGCCATAATAATAAGTGCTTTTAGAAAATTAATCATTTGTGTTTTTTTATGCATTTTGC 1675
Db |||||||
1977 CATGCCATAATAATAAGTGCTTTTAGAAAATTAATCATTTGTGTTTTTTTATGCATTTTGC 2036
QY 1676 TGAGGCATCCTTATTATTAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTTTATTA 1735
Db |||||||
2037 TGAGGCATCCTTATTATTAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTTTATTA 2096
QY 1736 TAGTCTTACAAAAGACAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTTCTTTGCAA 1795
Db |||||||
2097 TAGTCTTACAAAAGACAATGTATAAGCTGTAAACAGAAATTTTGAATTTGTTTTCTTTGCAA 2156
QY 1796 AACCCCTCCACAAAAGCAAATCCTTTCAAGAATGGCATGGGCATTTCTGTATGAACCTTTC 1855
Db |||||||
2157 AACCCCTCCACAAAAGCAAATCCTTTCAAGAATGGCATGGGCATTTCTGTATGAACCTTTC 2216
QY 1856 CAGATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACA 1915

Db ||||||| 2217 CAGATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACA 2276
QY 1916 TCGACGTAACCTGGAAA 1931
Db ||||||| 2277 TCGACGTAACCTGGAAA 2292
RESULT 13
ADQ23870
ID ADQ23870 standard; DNA; 4153 BP.
XX ADQ23870;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6690.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW ds.
XX Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX WPI; 2004-441208/41.
DR
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 6690; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 4153 BP; 1253 A; 855 C; 854 G; 1174 T; 0 U; 17 Other;
Query Match 98.0%; Score 1896.2; DB 12; Length 4153;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1911; Conservative 0; Mismatches 20; Indels 3; Gaps 1;
QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTCGAAAGGAAACGGCTACGTCAGAGTCCTAGA 60
Db ||||||| 602 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTCAGAGTCCTAGA 661
QY 61 TTCCCGAACAGTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 120
Db ||||||| 662 TTCCCGAACAGTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 721
QY 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180

|||||
722 ACACGGATACAGCTAGTGTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 781
QY
181 TGTAGGTATGATTTTGTGGAAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGA 240
Db
782 TGTAGGTATGATTTTGTGGAAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGA 841
QY
241 CGATGGTGTGGACACAAGGAAGTTCTTCCAAGGATATAAAATCAAGAACGAACCAAAATTAA 300
Db
842 CGATGGTGTGGACACAAGGAAGTTCTTCCAAGGATATAAAATCAAGAACGAACCAAAATTAA 901
QY
301 ATCACATTCAAGTCCGATCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 360
Db
902 ATCACATTCAAGTCCGATCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 961
QY
361 TTGCTGGAAGATTTCCAACCCGACGACGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 420
Db
962 TTGCTGGAAGATTTCCAACCCGACGACGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 1021
QY
421 TCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
Db
1022 TCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 1081
QY
481 GCTCTGGACAAAAAATTGCAGAAATTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 540
Db
1082 GCTCTGGACAAAAAATTGCAGAAATTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 1141
QY
541 CCAGAGTCAATGGCAAGAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db
1142 CCAGAGTCAATGGCAAGAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 1201
QY
601 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db
1202 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 1261
QY
661 CGTTACAGTTGCACTCCAGGAATTAATCGGTCAATATAAGAGAAAGCTGAAGTTGGCC 720
Db
1262 CGTTACAGTTGCACTCCAGGAATTAATCGGTCAATATAAGAGAAAGCTGAAGTTGGCC 1321
QY
721 AATGTGGTCTTCTTTCCAGTTGCCCTCGTCAGCGCTGTGGAGAAATTTGGCTGT 780
Db
1322 AATGTGGTCTTCTTTCCAGTTGCCCTCGTCAGCGCTGTGGAGAAATTTGGCTGT 1381
QY
781 GGAAGTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAACCCGTGAAAAAGTATCAT 840
Db
1382 GGAAGTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAACCCGTGAAAAAGTATCAT 1441
QY
841 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900
Db
1442 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 1501
QY
901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 960
Db
1502 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 1561
QY
961 CCTCGATAAGAGAAATGTCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020
Db
1562 CCTCGATAAGAGAAATGTCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1621
QY
1021 GGGTGAGATAAGAGACCCTTTTCTTACCAGCAACCAAACTTACTACTAGCTGCAATGCA 1080
Db
1622 GGGTGAGATAAGAGACCCTTTTCTTACCAGCAACCAAACTTACTACTAGCTGCAATGCA 1681
QY
1081 ATGAACACAAGTGGTTGCTGAGTCTCAGCCCTGCTTTGTTAATGCCATGGCAAGTAGAAA 1140
Db
1682 ATGAACACAAGTGGTTGCTGAGTCTCAGCCCTGCTTTGTTAATGCCATGGCAAGTAGAAA 1741
QY
1141 GGTATATCATCAACTTCTATACCTAAGAAATAGGATTGCATTTAATAATAGTGTGAG 1200
Db
1742 GGTATATCATCAACTTCTATACCTAAGAAATAGGATTGCATTTAATAATAGTGTGAG 1801
QY
1201 GTTATATATGCACAAACACACACAGAAATATATTCTATGTATATATAGATCAAAAT 1260
|||||

Db 1802 GTTATATATGCACAAACACACACAGAAATATATTATGTCTATGTATATATAGATCAAAAT 1861
QY 1261 GTTTTTTTTGGTATATATAACCAGGTACACCAGAGCTTACATATGTTTGGATTAGACTCT 1320
Db 1862 GTTTTTTTTGGTATATATAACCAGGTACACCAGAGCTTACATATGTTTGGATTAGACTCT 1921
QY 1321 TAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATT 1380
Db 1922 TAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATT 1981
QY 1381 AGGAGATAAAATTATTTTAAATTTTGAAACACAAAAACAATTTTGAATCTTGTCTCTTTA 1440
Db 1982 AGGAGATAAAATTATTTTAAATTTTGAAACACAAAAACAATTTTGAATCTTGTCTCTTTA 2041
QY 1441 AAGAAAGCATCTTGTATATTAAATAACAAAGATGAGGCTTTCTTACATATACATCTTAG 1500
Db 2042 AAGAAAGCATCTTGTATATTAAATAACAAAGATGAGGCTTTCTTACATATACATCTTAG 2101
QY 1501 TTGATTATTAATAAGGAAAAA ---GGTTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT 1557
Db 2102 TTGATTATTAATAAGGAAAAATATGGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT 2161
QY 1558 TTCCATGAGAAGCACTGCATACCTTACCTATGTGGACTGTAATAACCTGTCTCCAAAAACCA 1617
Db 2162 TTCCATGAGAAGCACTGCATACCTTACCTATGTGGACTATAATAACCTGTCTCCAAAAACCA 2221
QY 1618 TGCCATAATAATAAGTGCCTTTAGAAATTAATAATCATTTGTGTTTTTATGCAATTTTGTG 1677
Db 2222 TGCCATAATAATAAGTGCCTTTAGAAATTAATAATCATTTGTGTTTTTATGCAATTTTGTG 2281
QY 1678 AGGCATCCTTATTCATTTAACACCTATCTCAAAAAACCTTACTTAGAAGGTTTTTATTATA 1737
Db 2282 AGGCATGCTTATTCATTTAACACCTATCTCAAAAAACCTTACTTAGAAGGTTTTTATTATA 2341
QY 1738 GTCCTACAAAAAGACAATGTATAAGCTGTAACAGAAATTTTGAATGTTTTTCTTTGCAAAA 1797
Db 2342 GTCCTACAAAAAGACAATGTATAAGCTGTAACAGAAATTTTGAATGTTTTTCTTTGCAAAA 2401
QY 1798 CCCCTCCACAAAAAGCAAAATCCTTTCAAGAATGGCATGGGCAATCTGTATGAAACCTTTCCA 1857
Db 2402 CCCCTCCACAAAAAGCAAAATCCTTTCAAGAATGGCATGGGCAATCTGTATNNNNNNNNN 2461
QY 1858 GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAAACATTGAAACATC 1917
Db 2462 NNNNNNGTTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAAACATTGAAACATC 2521
QY 1918 GACGTAACCTGAAA 1931
Db 2522 GACGTAACCTGAAA 2535

RESULT 14

ADQ22990
ID ADQ22990 standard; DNA; 4153 BP.
XX

AC ADQ22990;

XX
DT 26-AUG-2004 (first entry)

XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5810.

XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
ds.

XX
OS Homo sapiens.

XX
PN WO2004048938-A2.

XX
PD 10-JUN-2004.

XX
PF 26-NOV-2003; 2003WO-US038193.

XX
PR 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.
XX PA
XX Aziz N, Ginsburg WM, Zlotnik A;
XX WPI; 2004-441208/41.
XX
XX Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX PT and comparing the gene expression, also useful in treating soft tissue
XX PT sarcoma.
XX PT
XX PS Example 2; SEQ ID NO 5810; 210pp; English.
XX
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX CC and a normal soft tissue sample from the same or different individual,
XX CC determining the expression of a gene in both samples and comparing the
XX CC expression of the gene in both soft tissue samples, where a higher level
XX CC of protein expression in the first soft tissue sample indicates the
XX CC presence of soft tissue sarcoma. The method of the invention has
XX CC cytotstatic applications and may be useful for detecting soft tissue
XX CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX CC acid sequences may be useful in diagnostic and screening applications.
XX CC The current sequence is that of a human soft tissue sarcoma-upregulated
XX CC DNA of the invention. The current sequence is not shown within the
XX CC specification per se but was submitted in CD format by the inventor.
XX
XX SQ Sequence 4153 BP; 1253 A; 855 C; 854 G; 1174 T; 0 U; 17 Other;
Query Match 98.0%; Score 1896.2; DB 12; Length 4153;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1911; Conservative 0; Mismatches 20; Indels 3; Gaps 1;
1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGATCCTAGA 60
602 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGATCCTAGA 661
61 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACCTCTCAGGAGAA 120
662 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACCTCTCAGGAGAA 721
121 ACACGGATACAGCTAGTGTGACAAATCAGTTTGGATTAGAGGAAGCAGAGAAATGATATC 180
722 ACACGGATACAGCTAGTGTGACAAATCAGTTTGGATTAGAGGAAGCAGAGAAATGATATC 781
181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATAGAGGA 240
782 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATAGAGGA 841
241 CGATGGTGTGGACACAAAGGAAGTTCCCTCAAGGATAAAATCAAGAACGAAACCAAAATAAA 300
842 CGATGGTGTGGACACAAAGGAAGTTCCCTCAAGGATAAAATCAAGAACGAAACCAAAATAAA 901
301 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATATTCT 360
902 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATATTCT 961
361 TTGCTGGAAGATTTCCRAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAGC 420
962 TTGCTGGAAGATTTCCRAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAGC 1021
421 TCTATTTCCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
1022 TCTATTTCCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 1081
481 GCTCTGGACAAAAAATGACAGAAATTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 540
1082 GCTCTGGACAAAAAATGACAGAAATTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 1141
541 CCAGAGTCA TGGCAAGAGATCTTGGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 600
1142 CCAGAGTCA TGGCAAGAGATCTTGGAGAAATATGATCTGGACACCCCTCGGTATCGAGGC 1201

QY 601 AGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 1202 AGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 1261
QY 661 CGTTACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC 720
Db 1262 CGTTACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC 1321
QY 721 AATGTGGTCTTCTTTCCACGTTGCCCTCCTCTGTCAGCGCTGTGGAGGAAATTTGGCTGT 780
Db 1322 AATGTGGTCTTCTTTCCACGTTGCCCTCCTCTGTCAGCGCTGTGGAGGAAATTTGGCTGT 1381
QY 781 GGAACGTCAACTGGAGGTCTGTCACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 840
Db 1382 GGAACGTCAACTGGAGGTCTGTCACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 1441
QY 841 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGAGGAGGGGTAGAGCTAAGACCATGGCT 900
Db 1442 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGAGGAGGGGTAGAGCTAAGACCATGGCT 1501
QY 901 CTAGTTGACATCCAGTTGGATCACCATGACGATCCGATTGTATCTGACGCTCAAGACCA 960
Db 1502 CTAGTTGACATCCAGTTGGATCACCATGACGATGTGATTGTATCTGACGCTCAAGACCA 1561
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Db 1562 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1621
QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1080
Db 1622 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1681
QY 1081 ATGAACACAAAGTGGTGTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1140
Db 1682 ATGAACACAAAGTGGTGTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1741
QY 1141 GGTATATCATCAACTTCTATACCTTAAGAATATAGGATTGCAATTTAATAATAGTGTGAG 1200
Db 1742 GGTATATCATCAACTTCTATACCTTAAGAATATAGGATTGCAATTTAATAATAGTGTGAG 1801
QY 1201 GTTATATATGCACAAAACACACACAGAAATATATTCTATGTCTATGTGTATATAGATCAAAT 1250
Db 1802 GTTATATATGCACAAAACACACACAGAAATATATTCTATGTCTATGTGTATATAGATCAAAT 1861
QY 1261 GTTTTTTTTGTGTATATATAACCAGGTACACCCAGAGCTTACATATGTTGAGTTAGACTCT 1320
Db 1862 GTTTTTTTTGTGTATATATAACCAGGTACACCCAGAGCTTACATATGTTGAGTTAGACTCT 1921
QY 1321 TAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT 1380
Db 1922 TAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT 1981
QY 1381 AGGAGATAAATTTATTTTAAATTTTGAAACACAAAACAATTTTGAATCTTGCTCTCTTA 1440
Db 1982 AGGAGATAAATTTATTTTAAATTTTGAAACACAAAACAATTTTGAATCTTGCTCTCTTA 2041
QY 1441 AAGAAAGCATCTTGATATATAAATAATCAAAAAGATGAGGCTTTCTTACATATACATCTTAG. 1500
Db 2042 AAGAAAGCATCTTGATATATAAATAATCAAAAAGATGAGGCTTTCTTACATATACATCTTAG. 2101
QY 1501 TTGATTATTAAAAAAGGAAAAA ---GGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT 1557
Db 2102 TTGATTATTAAAAAAGGAAAAAATATGGTTTCCAGAGAAAAAGGCCAATACCTAAGCATTTT 2161
QY 1558 TTCCATGAGAGCACTGCATACCTTACCTATGTGGA CTGTAATAACCTGTCTCCAAAACCA 1617
Db 2162 TTCCATGAGAGCACTGCATACCTTACCTATGTGGA CTATATAAACCTGTCTCCAAAACCA 2221
QY 1618 TGCCATAATAATAAGTGTCTTTAGAAAATTAAATCATTTGTGTTTTTTTATGCAATTTTGCTG 1677
Db 2222 TGCCATAATAATAAGTGTCTTTAGAAAATTAAATCATTTGTGTTTTTTTATGCAATTTTGCTG 2281

QY 1678 AGGCATCCTTATTCAATTAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTTATTATA 1737
|||||
Db 2282 AGGCATGCTTATTCAATTAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTTATTATA 2341

QY 1738 GTCCTACAAAAACAAATGTATAAGCTGTAAACAGAAATTTTGAATTGTTTTTCTTTGCAAAA 1797
|||||
Db 2342 GTCCTACAAAAACAAATGTATAAGCTGTAAACAGAAATTTTGAATTGTTTTTCTTTGCAAAA 2401

QY 1798 CCCCTCACAAAAAGCAAATCCTTTCAAGAAATGGCATGGGCATTTCTGTATGAACCTTTCCA 1857
|||||
Db 2402 CCCCTCACAAAAAGCAAATCCTTTCAAGAAATGGCATGGGCATTTCTGTATNNNNNNNNN 2461

QY 1858 GATGGTTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAAACATTGAAACATC 1917
|||||
Db 2462 NNNNNGTTCAAGTGAAGAGATGTGGGTAGTTGAGAACTTAAAAAGTGAAACATTGAAACATC 2521

QY 1918 GACGTAACGTGAAA 1931
|||||
Db 2522 GACGTAACGTGAAA 2535

RESULT 15
ADQ24013
ID ADQ24013 standard; DNA; 4153 BP.
AC ADQ24013;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6833.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW ds.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
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PS Example 2; SEQ ID NO 6833; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytotostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.
SQ Sequence 4153 BP; 1253 A; 855 C; 854 G; 1174 T; 0 U; 17 Other;

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Matches 1911; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAAGGAAACGGCTACGTGAGAGTCTCTAGA 60
Db 602 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAAGGAAACGGCTACGTGAGAGTCTCTAGA 661

QY 61 TTCCCGAACAGCTACCCCGAGGAACCTCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 120
Db 662 TTCCCGAACAGCTACCCCGAGGAACCTCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 721

QY 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180
Db 722 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 781

QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAAGATATATCCGAAACCAAGTACCATTATTAGAGGA 240
Db 782 TGTAGGTATGATTTTGTGGAAGTTGAAAGATATATCCGAAACCAAGTACCATTATTAGAGGA 841

QY 241 CGATGGTGTGGACACAAAGGAAGTTCTCTCAAGGATAAAATCAAGAACCAACCAATTTAA 300
Db 842 CGATGGTGTGGACACAAAGGAAGTTCTCTCAAGGATAAAATCAAGAACCAACCAATTTAA 901

QY 301 ATCACATTTCAAGTCCGATGACTACTTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 360
Db 902 ATCACATTTCAAGTCCGATGACTACTTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 961

QY 361 TTGCTGGAAGATTTCCAAACCCGACAGCTTCAGAGACCAACTGGGAATCTGTCACAAGC 420
Db 962 TTGCTGGAAGATTTCCAAACCCGACAGCTTCAGAGACCAACTGGGAATCTGTCACAAGC 1021

QY 421 TCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACCTCTGATTGCGGAT 480
Db 1022 TCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACCTCTGATTGCGGAT 1081

QY 481 GCTCTGGACAAAAAATTTGCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540
Db 1082 GCTCTGGACAAAAAATTTGCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 1141

QY 541 CCAGAGTCATGGCAAGAAGATCTTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 1142 CCAGAGTCATGGCAAGAAGATCTTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC 1201

QY 601 AGGTCATACCATGACCCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 1202 AGGTCATACCATGACCCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 1261

QY 661 CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAAAGCTGAAGTTGGCC 720
Db 1262 CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAAAGCTGAAGTTGGCC 1321

QY 721 AATGTGGTCTTCTTTCCACGTTGCCCTCCTCGTGACGCGCTGTGGAGGAAATTTGTGGCTGT 780
Db 1322 AATGTGGTCTTCTTTCCACGTTGCCCTCCTCGTGACGCGCTGTGGAGGAAATTTGTGGCTGT 1381

QY 781 GGAACCTGTCAACTGGAGGTCTCTGCACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 840
Db 1382 GGAACCTGTCAACTGGAGGTCTCTGCACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 1441

QY 841 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900
Db 1442 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 1501

QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGACGCTCAAGACCA 960
Db 1502 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGACGCTCAAGACCA 1561

QY 961 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020
Db 1562 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1621

QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1080

| | | | |
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| Db | 1622 | GGGTGAGATAAGAGACCCCTTTTCCTACCAGCAACCAACTTACTAGCCTGCAATGCA | 1681 |
| Qy | 1081 | ATGAACACAAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA | 1140 |
| Db | 1682 | ATGAACACAAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA | 1741 |
| Qy | 1141 | GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCATTTAATAATAGTGTGAG | 1200 |
| Db | 1742 | GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCATTTAATAATAGTGTGAG | 1801 |
| Qy | 1201 | GTTATATATGCACAAAACACACACAGAAAATATATTCACTGTCTATGTGTATATAGATCAAAAT | 1260 |
| Db | 1802 | GTTATATATGCACAAAACACACACAGAAAATATATTCACTGTCTATGTGTATATAGATCAAAAT | 1861 |
| Qy | 1261 | GTTTTTTGTGGTATATATAACCAGGTACACCAGAGCTTACATATGTTTGAGTTAGACTCT | 1320 |
| Db | 1862 | GTTTTTTGTGGTATATATAACCAGGTACACCAGAGCTTACATATGTTTGAGTTAGACTCT | 1921 |
| Qy | 1321 | TAAATCCTTTGCCAAAAATAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT | 1380 |
| Db | 1922 | TAAATCCTTTGCCAAAAATAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAAATTT | 1981 |
| Qy | 1381 | AGGAGATAAAATTTATTTTAAATTTTGAAACACAAAACAAATTTTGAATCTTGCTCTCTTA | 1440 |
| Db | 1982 | AGGAGATAAAATTTATTTTAAATTTTGAAACACAAAACAAATTTTGAATCTTGCTCTCTTA | 2041 |
| Qy | 1441 | AAGAAAGCATCTTGATATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG | 1500 |
| Db | 2042 | AAGAAAGCATCTTGATATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG | 2101 |
| Qy | 1501 | TTGATTATTAATAAGGAAAAA--GGTTTCCAGAGAAAAAGGCCAATACCTAGCATTTT | 1557 |
| Db | 2102 | TTGATTATTAATAAGGAAAAAATATGGTTTCCAGAGAAAAAGGCCAATACCTAGCATTTT | 2161 |
| Qy | 1558 | TTCCATGAGAAGCACTGCATACTTACCTATGTGGACTGTAATAACCTGTCTCCAAAACCA | 1617 |
| Db | 2162 | TTCCATGAGAAGCACTGCATACTTACCTATGTGGACTATAATAACCTGTCTCCAAAACCA | 2221 |
| Qy | 1618 | TGCCATAATAATAAGTGTCTTTAGAAATTAAATCATTTGTTTTTTTATGCATTTTGCTG | 1677 |
| Db | 2222 | TGCCATAATAATAAGTGTCTTTAGAAATTAAATCATTTGTTTTTTTATGCATTTTGCTG | 2281 |
| Qy | 1678 | AGGCATCCTTATTCAATTTAACACCTATCTCAAAAACCTTACTTAGAAGTTTTTTATTATA | 1737 |
| Db | 2282 | AGGCATGCTTATTCAATTTAACACCTATCTCAAAAACCTTACTTAGAAGTTTTTTATTATA | 2341 |
| Qy | 1738 | GTCCTACAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTCTTTTGCAAAA | 1797 |
| Db | 2342 | GTCCTACAAAAGACAAATGTATAAGCTGTAAACAGAAATTTTGAATTTCTTTTGCAAAA | 2401 |
| Qy | 1798 | CCCCTCCACAAAAGCAATCCTTTCAAGAATGGCATGGGCATTTCTGTATGAACCTTTCCA | 1857 |
| Db | 2402 | CCCCTCCACAAAAGCAATCCTTTCAAGAATGGCATGGGCATTTCTGTATNNNNNNNNN | 2461 |
| Qy | 1858 | GATGGTGTTCAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACATC | 1917 |
| Db | 2462 | NNNNNGTTCAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACATC | 2521 |
| Qy | 1918 | GACGTAACCTGGAAA | 1931 |
| Db | 2522 | GACGTAACCTGGAAA | 2535 |

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OM protein - protein search, using sw model

Run on: October 29, 2004, 23:15:13 ; Search time 158 Seconds
(without alignments)
731.081 Million cell updates/sec

Title: US-10-086-623-6
Perfect score: 1742
Sequence: 1 LYRRDETIQKNGYVQSPR.....DIQLDHERCDCICSSRPPR 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1742 | 100.0 | 322 | 3 | AAY71129 Human Pla |
| 2 | 1742 | 100.0 | 347 | 7 | ADK68120 Novel NOV |
| 3 | 1742 | 100.0 | 364 | 4 | AAU12264 Human PRO |
| 4 | 1742 | 100.0 | 364 | 5 | AAE15820 Human LP8 |
| 5 | 1742 | 100.0 | 364 | 5 | ABB84973 Human PRO |
| 6 | 1742 | 100.0 | 364 | 5 | ABB95579 Human ang |
| 7 | 1742 | 100.0 | 364 | 6 | ABO17708 Novel hum |
| 8 | 1742 | 100.0 | 364 | 6 | ABU80962 Human PRO |
| 9 | 1742 | 100.0 | 364 | 6 | ABU66662 Human PRO |
| 10 | 1742 | 100.0 | 364 | 6 | ABU59743 Novel sec |
| 11 | 1742 | 100.0 | 364 | 6 | ABO24933 Human sec |
| 12 | 1742 | 100.0 | 364 | 6 | ABU66938 Human sec |
| 13 | 1742 | 100.0 | 364 | 6 | ADA45705 Novel hum |
| 14 | 1742 | 100.0 | 364 | 6 | ADA76136 Human PRO |
| 15 | 1742 | 100.0 | 364 | 6 | ADA18786 Human PRO |
| 16 | 1742 | 100.0 | 364 | 6 | ADA61409 Homo sapi |
| 17 | 1742 | 100.0 | 364 | 6 | ADB19194 Novel hum |
| 18 | 1742 | 100.0 | 364 | 6 | ADB27735 Human PRO |
| 19 | 1742 | 100.0 | 364 | 6 | ADA86214 Novel hum |
| 20 | 1742 | 100.0 | 364 | 6 | ADB15778 Human PRO |
| 21 | 1742 | 100.0 | 364 | 6 | ADA47564 Human PRO |
| 22 | 1742 | 100.0 | 364 | 6 | ADA67359 Human PRO |
| 23 | 1742 | 100.0 | 364 | 6 | ADB30366 Human PRO |
| 24 | 1742 | 100.0 | 364 | 6 | ADA85662 Novel hum |
| 25 | 1742 | 100.0 | 364 | 6 | ADA96874 Human PRO |

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| 26 | 1742 | 100.0 | 364 | 6 | ADA79178 | Ada79178 Human PRO |
| 27 | 1742 | 100.0 | 364 | 6 | ADA87317 | Ada87317 Novel hum |
| 28 | 1742 | 100.0 | 364 | 6 | ADB16519 | Adb16519 Human PRO |
| 29 | 1742 | 100.0 | 364 | 6 | ADA91611 | Ada91611 Novel hum |
| 30 | 1742 | 100.0 | 364 | 6 | ADB14674 | Adb14674 Human PRO |
| 31 | 1742 | 100.0 | 364 | 6 | ADB18635 | Adb18635 Novel hum |
| 32 | 1742 | 100.0 | 364 | 6 | ADA93850 | Ada93850 Human PRO |
| 33 | 1742 | 100.0 | 364 | 6 | ADB19746 | Adb19746 Novel hum |
| 34 | 1742 | 100.0 | 364 | 6 | ADB13058 | Adb13058 Human PRO |
| 35 | 1742 | 100.0 | 364 | 6 | ABO43241 | Abo43241 Novel hum |
| 36 | 1742 | 100.0 | 364 | 6 | ADA74312 | Ada74312 Human PRO |
| 37 | 1742 | 100.0 | 364 | 6 | ADB24545 | Adb24545 Human PRO |
| 38 | 1742 | 100.0 | 364 | 6 | ADA82069 | Ada82069 Human PRO |
| 39 | 1742 | 100.0 | 364 | 6 | ADA75032 | Ada75032 Human PRO |
| 40 | 1742 | 100.0 | 364 | 6 | ADA85110 | Ada85110 Novel hum |
| 41 | 1742 | 100.0 | 364 | 6 | ADA84558 | Ada84558 Novel hum |
| 42 | 1742 | 100.0 | 364 | 6 | ADB29814 | Adb29814 Human PRO |
| 43 | 1742 | 100.0 | 364 | 6 | ADA80342 | Ada80342 Human PRO |
| 44 | 1742 | 100.0 | 364 | 6 | ADA75584 | Ada75584 Human PRO |
| 45 | 1742 | 100.0 | 364 | 6 | ADA46809 | Ada46809 Human PRO |

ALIGNMENTS

RESULT 1
AAY71129
ID AAY71129 standard; peptide; 322 AA.
XX
AC AAY71129;
XX
DT 08-SEP-2000 (first entry)
XX
DE Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #2.
XX
KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary;
KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
KW proliferative; activator; proliferation; differentiation; motility;
KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
KW atherosclerosis; wound; metastasis.
XX Homo sapiens.
OS
XX
PN WO200027879-A1.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-US026462.
XX
PR 10-NOV-1998; 98US-0107852P.
PR 28-DEC-1998; 98US-0113997P.
PR 26-AUG-1999; 99US-0150604P.
PR 04-OCT-1999; 99US-0157108P.
PR 05-OCT-1999; 99US-0157756P.
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;
PI Oestman A, Heldin C;
XX
DR WPI; 2000-376495/32.
DR N-PSDB; AAD00737.
XX
PT Novel polynucleotides encoding a novel growth factor of cells expressing
PT a platelet-derived growth factor, useful for diagnostic and therapeutic
PT applications, e.g. concerning cancer.
XX
PS Claim 25; Fig 6; 11pp; English.
XX
CC The present sequence is an N-terminally truncated polypeptide of human
CC platelet derived growth factor (PDGF)-D, formally known as Vascular
CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung

CC lambdagtl0 cDNA library. It belongs to the VEGF/PDGF family. It functions
CC as an activator of proliferation, differentiation, growth and motility of
CC cells, that express PDGF-D receptor. This sequence is useful for
CC inhibiting the growth of tumours, that express PDGF-D. Expression of PDGF
CC -D and its proteolytic cleavage for generating an activated truncated
CC form is useful for regulating receptor binding specificity of PDGF-D.
CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the
CC invasion of tumour cells into normal cells. PDGF-D may be used to treat
CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells
XX
SQ Sequence 322 AA;

Query Match 100.0%; Score 1742; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.1e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Qy 61 CRYDFVEVEDISETSTIIIRGRWCCHKVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 CRYDFVEVEDISETSTIIIRGRWCCHKVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 120
Qy 121 LLEDFOQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 LLEDFOQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN 180
Qy 181 PESWQEDLENMYLDTPRYGRGRSYHDKSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 PESWQEDLENMYLDTPRYGRGRSYHDKSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA 240
Qy 241 NVVFFPRCLLVORCGNGCGGTVNWRSCTCNSGKTVKXYHEVLQFEPGHKIRGRAKTMA 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 NVVFFPRCLLVORCGNGCGGTVNWRSCTCNSGKTVKXYHEVLQFEPGHKIRGRAKTMA 300
Qy 301 LVDIQLDHHERCDCICSSRP 322
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 LVDIQLDHHERCDCICSSRP 322

RESULT 2
ADK68120
ID ADK68120 standard; protein; 347 AA.
XX
AC ADK68120;
XX
DT 06-MAY-2004 (first entry)
XX
DE Novel NOVX protein #23.
XX
KW antidiabetic; anorectic; cardiac; hypotensive; antiarteriosclerotic;
KW anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
KW antiarthritic; antiinflammatory; dermatological; antiasthmatic;
KW antilipemic; gene therapy; metabolic disorder; diabetes; obesity;
KW infectious disease; anorexia; cancer; cardiovascular disease;
KW hypertension; atherosclerosis; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW osteoarthritis; hematopoietic disorders; inflammatory skin disorder;
KW asthma; dyslipidemia; neurogenesis; cell differentiation;
KW cell proliferation; hematopoiesis; wound healing; angiogenesis;
KW chromosome mapping; pharmacogenomic.

OS Homo sapiens.
XX
PN WO2003085124-A2.
XX
PD 16-OCT-2003.
XX
PF 01-APR-2003; 2003WO-US009775.
XX
PR 01-APR-2002; 2002US-0369065P.

PR 05-APR-2002; 2002US-0370279P.
PR 05-APR-2002; 2002US-0370359P.
PR 08-APR-2002; 2002US-0370969P.
PR 12-APR-2002; 2002US-0372019P.
PR 22-APR-2002; 2002US-0374379P.
PR 15-MAY-2002; 2002US-0380973P.
PR 30-MAY-2002; 2002US-0384297P.
PR 30-MAY-2002; 2002US-0384329P.
PR 17-JUN-2002; 2002US-0389729P.
PR 13-AUG-2002; 2002US-0403491P.
PR 15-AUG-2002; 2002US-0403748P.
PR 31-MAR-2003; 2003US-00403142.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Bento P, Boldog FL, Burgess CE, Casman SJ;
PI Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes ER, Gerlach VL;
PI Grosse WM, Gunther E, Gusev VY, Heyes MP, Lepley DM, Li L;
PI Macdougall JR, Malyankar UM, Millet I, Patturajan M, Peyman JA;
PI Rastelli L, Rieger DK, Shenoy SG, Shinkets RD, Smithson G, Stone DJ;
PI Vernet CAM, Voss EZ;
DR WPI; 2003-812730/76.
DR N-PSDB; ADK68119.
XX
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
PS Claim 1; SEQ ID NO 46; 323pp; English.

CC The invention relates to novel NOVX protein and their encoding DNA's,
CC mature forms of the proteins or sequences that are at least 95% identical
CC to, or having one or more conservative amino acid substitutions in, the
CC proteins. The polypeptides, nucleic acid molecules and antibodies are
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), hematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidemias. The nucleic acids and polypeptides may
CC also be used as targets for the identification of small molecules that
CC modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC corresponds to one of the NOVX proteins of the invention.

SQ Sequence 347 AA;

Query Match 100.0%; Score 1742; DB 7; Length 347;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Dy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
26 LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 85
Qy 61 CRYDFVEVEDISETSTIIIRGRWCCHKVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 120
Dy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
86 CRYDFVEVEDISETSTIIIRGRWCCHKVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 145
Qy 121 LLEDFOQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN 180
Dy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
146 LLEDFOQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN 205

QY 181 PESWQEDLENMYLDTPRYGRGRSYHDKRSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA 240
Db |||||||
QY 206 PESWQEDLENMYLDTPRYGRGRSYHDKRSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA 265
Db |||||||
QY 241 NVVFFPRCLLVQRCGCGGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db |||||||
QY 266 NVVFFPRCLLVQRCGCGGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 325
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db |||||||
QY 326 LVDIQLDHHERCDCICSSRPPR 347
RESULT 3
AAU12264
ID AAU12264 standard; protein; 364 AA.
XX
AC AAU12264;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO4345 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN W0200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21336.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 186; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane.PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 364 AA;

Query Match 100.0%; Score 1742; DB 4; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRRDETIQKNGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db |||||||
QY 43 LYRRDETIQKNGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 102
QY 61 CRYDFVEVEDISSETIIRGRCGKHKEVPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db |||||||
QY 103 CRYDFVEVEDISSETIIRGRCGKHKEVPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDFOQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN 180
Db |||||||
QY 163 LLEDFOQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRGRSYHDKRSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA 240
Db |||||||
QY 223 PESWQEDLENMYLDTPRYGRGRSYHDKRSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA 282
QY 241 NVVFFPRCLLVQRCGCGGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db |||||||
QY 283 NVVFFPRCLLVQRCGCGGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 342
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db |||||||
QY 343 LVDIQLDHHERCDCICSSRPPR 364

RESULT 4
AAE15820

ID XX AAE15820 standard; protein; 364 AA.

AC XX AAE15820;

XX DT 26-MAR-2002 (first entry)

XX DE Human LP85 protein #2.

KW LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulnerary; osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder; MSD; therapy; bone growth; cartilage differentiation; wound healing; neuron growth; bone fracture; osteoporosis; osteopenia; arthritis; sarcopenia; periodontal disease; tissue atrophy; endocrine disorder; muscle loss; immobility; bone density.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1. .12

FT /label= Signal_peptide

FT Protein 13. .364

FT /label= Human_mature_LP85_protein

XX WO200189450-A2.

PN 29-NOV-2001.

PD 08-MAY-2001; 2001WO-US011755.

XX 19-MAY-2000; 2000US-0205424P.

PR 11-JAN-2001; 2001US-0261071P.

PR 11-JAN-2001; 2001US-0261076P.

XX (ELIL) LILLY & CO ELI.

XX Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;

PI Witcher DR, Wroblewski VJ;

XX WPI; 2002-083040/11.

DR N-PSDB; AAD25489.

XX Analog of a platelet-derived growth factor homolog, LP85 useful for treating osteoporosis, arthritis, sarcopenia, wounds, has one or more amino acid substitutions which destroy the tripeptidyl sequence of native LP85.

XX Disclosure; Page 114-115; 117pp; English.

XX The present invention relates to LP85, an analogue of platelet-derived growth factor (PDGF) homologue. Sequences of the invention are useful for the manufacture of a medicament for treating musculoskeletal disorder (MSD) which include promoting bone growth, cartilage differentiation and function, wound healing, neuron growth, preventing cartilage degradation or neuronal degeneration. They are useful for treating bone fractures, osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease, tissue atrophy, traumatised connective tissues, grafted connective tissues and/or transplanted organs, bone or muscle loss due to malignancy, endocrine disorders and immobility. They are also used for prophylactically increasing or maintaining bone density in a mammal. The present sequence is human LP85 protein

XX Sequence 364 AA;

Query Match 100.0%; Score 1742; DB 5; Length 364;

Best Local Similarity 100.0%; Pred. No. 5e-166;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LYRDETIQVKNGYVQSPRFPNSYPNRLLLTWRLHSENTRIQLVFDNQFGLAEAENDI 60

DB 43 LYRDETIQVKNGYVQSPRFPNSYPNRLLLTWRLHSENTRIQLVFDNQFGLAEAENDI 102

OY 61 CRYDFVEVEDISETSTIIRGWCCHKVEVPPRIKSRTNQIKITFKSDDDYFVAKPGFKIYYS 120

Db 103 CRYDFVEVEDISETSTIIRGWCCHKVEVPPRIKSRTNQIKITFKSDDDYFVAKPGFKIYYS 162

OY 121 LLEDFOPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 180

Db 163 LLEDFOPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 222

OY 181 PESWQEDLENMYLDTPRYRGRSYHDKRSKVDLDRLNDDAKRYSCPTPRNYSVNIREELKLA 240

Db 223 PESWQEDLENMYLDTPRYRGRSYHDKRSKVDLDRLNDDAKRYSCPTPRNYSVNIREELKLA 282

OY 241 NVVFFPRCLLVORCGGCGGTVNWRSCNCGTKVKKYHEVLQFEPGHIKRRGRAKTMA 300

Db 283 NVVFFPRCLLVORCGGCGGTVNWRSCNCGTKVKKYHEVLQFEPGHIKRRGRAKTMA 342

OY 301 LVDIQLDHHERCDCICSSRPPR 322

Db 343 LVDIQLDHHERCDCICSSRPPR 364

RESULT 5

ABB84973

ID ABB84973 standard; protein; 364 AA.

XX ABB84973;

XX 16-MAY-2002 (first entry)

DE Human PRO4345 protein sequence SEQ ID NO:314.

XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.

XX Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

PF 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220664P.

PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.

PR 17-AUG-2000; 2000US-00643657.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-00664610.

PR 18-SEP-2000; 2000US-00665350.

PR 24-OCT-2000; 2000US-0242922P.

PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 22-JAN-2001; 2001US-00767609.

PR 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00808689.

PR 22-MAR-2001; 2001US-00816744.

PR 05-APR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX (GETH) GENENTECH INC.
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Paoni NF;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Ye W;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-090516/12.
DR N-PSDB; ABL88228.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 314; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 364 AA;

Query Match 100.0%; Score 1742; DB 5; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRRDETIQVKNGYVQSPRFPNSYPRNLLTWRLHSQENTRIQLVFNQFGLAEAENDI 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
43 LYRRDETIQVKNGYVQSPRFPNSYPRNLLTWRLHSQENTRIQLVFNQFGLAEAENDI 102
QY 61 CRYDFVEVEDISSETIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
103 CRYDFVEVEDISSETIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDFOAAAASETWNESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVDDLKYFN 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
163 LLEDFOAAAASETWNESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVDDLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRSYHDKRSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
223 PESWQEDLENMYLDTPRYGRSYHDKRSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 282
QY 241 NVVFFPRCLLVQRCGCGCGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
283 NVVFFPRCLLVQRCGCGCGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 342
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
343 LVDIQLDHHERCDCICSSRPPR 364

RESULT 6
ABB95579
ID ABB95579 standard; protein; 364 AA.

XX ABB95579;
AC 19-JUL-2002 (first entry)
XX
DT Human angiogenesis related protein PRO4345 SEQ ID NO: 314.
XX
DE Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic;
XX Homo sapiens.
OS WO200208284-A2.
XX 31-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-US021735.
PF 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95717.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 314; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
SQ Sequence 364 AA;

Query Match 100.0%; Score 1742; DB 5; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRDETQVKGNGYVQSPFPNSYPNRLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db |||||
QY 43 LYRDETQVKGNGYVQSPFPNSYPNRLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 102
Db |||||
QY 61 CRYDFVEVEDISETSTIIRGRWCCHKKEVPPIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db |||||
QY 103 CRYDFVEVEDISETSTIIRGRWCCHKKEVPPIKSRTNQIKITFKSDDYFVAKPGFKIYYS 162
Db |||||
QY 121 LLEDQPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 180
Db |||||
QY 163 LLEDQPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 222
Db |||||
QY 181 PESWQEDLENMYLDTPRYGRGRSYHDKRSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA 240
Db |||||
QY 223 PESWQEDLENMYLDTPRYGRGRSYHDKRSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA 282
Db |||||
QY 241 NVVFFPRCLLVQRCGNGCGGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db |||||
QY 283 NVVFFPRCLLVQRCGNGCGGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 342
Db |||||
QY 301 LVDIQLDHERCDCICSSRPPR 322
Db |||||
QY 343 LVDIQLDHERCDCICSSRPPR 364
Db |||||

RESULT 7
ABO17708
ID ABO17708 standard; protein; 364 AA.
XX
AC ABO17708;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO4345.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.

XX Homo sapiens.
OS US2003032156-A1.
XX
PN 13-FEB-2003.
XX
PD 06-MAY-2002; 2002US-00140474.
XX
PF 31-MAR-1997; 97WO-US005230.
XX 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-341980/32.
DR N-PSDB; ACD23945.
XX
PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 186; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and

CC transmembrane PRO polypeptide
XX
SQ Sequence 364 AA;
Query Match 100.0%; Score 1742; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDI 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
43 LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDI 102
QY 61 CRYDFVEVEDISETSTIIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
103 CRYDFVEVEDISETSTIIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDFOAAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
163 LLEDFOAAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLDRNLDDAKRYSCTPRNYSVNIREELKLA 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
223 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLDRNLDDAKRYSCTPRNYSVNIREELKLA 282
QY 241 NVVFFPRCLLVQRCGGNCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHKRRGRAKTMA 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
283 NVVFFPRCLLVQRCGGNCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHKRRGRAKTMA 342
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
343 LVDIQLDHHERCDCICSSRPPR 364
RESULT 8
ABU80962
ID ABU80962 standard; protein; 364 AA.
XX
AC ABU80962;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human PRO polypeptide #93.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
KW antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;
KW antirheumatic; auditory; cerebroprotective; angiogenic.
XX
OS Homo sapiens.
XX
PN US2003004311-A1.
XX
PD 02-JAN-2003.
XX
PF 19-DEC-2001; 2001US-00028072.
XX
PR 18-JUN-1997; 97US-0049911P.
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059352P.
PR 19-SEP-1997; 97US-0059588P.
PR 24-SEP-1997; 97US-0059836P.
PR 17-OCT-1997; 97US-0062250P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.

| | | |
|----|--------------|----------------|
| PR | 17-OCT-1997; | 97US-0063755P; |
| PR | 24-OCT-1997; | 97US-0062814P; |
| PR | 24-OCT-1997; | 97US-0062816P; |
| PR | 24-OCT-1997; | 97US-0063045P; |
| PR | 24-OCT-1997; | 97US-0063082P; |
| PR | 24-OCT-1997; | 97US-0063127P; |
| PR | 27-OCT-1997; | 97US-0063327P; |
| PR | 27-OCT-1997; | 97US-0063329P; |
| PR | 28-OCT-1997; | 97US-0063550P; |
| PR | 28-OCT-1997; | 97US-0063561P; |
| PR | 29-OCT-1997; | 97US-0063704P; |
| PR | 29-OCT-1997; | 97US-0063733P; |
| PR | 29-OCT-1997; | 97US-0063735P; |
| PR | 29-OCT-1997; | 97US-0063738P; |
| PR | 03-NOV-1997; | 97US-0064248P; |
| PR | 07-NOV-1997; | 97US-0064809P; |
| PR | 12-NOV-1997; | 97US-0065186P; |
| PR | 17-NOV-1997; | 97US-0065846P; |
| PR | 21-NOV-1997; | 97US-0066364P; |
| PR | 24-NOV-1997; | 97US-0066453P; |
| PR | 24-NOV-1997; | 97US-0066511P; |
| PR | 24-NOV-1997; | 97US-0066770P; |
| PR | 11-DEC-1997; | 97US-0069212P; |
| PR | 11-DEC-1997; | 97US-0069278P; |
| PR | 11-DEC-1997; | 97US-0069334P; |
| PR | 16-DEC-1997; | 97US-0069694P; |
| PR | 23-JAN-1998; | 98US-0072320P; |
| PR | 04-FEB-1998; | 98US-0073612P; |
| PR | 09-FEB-1998; | 98US-0074086P; |
| PR | 09-FEB-1998; | 98US-0074092P; |
| PR | 12-MAR-1998; | 98US-0077791P; |
| PR | 20-MAR-1998; | 98US-0078910P; |
| PR | 25-MAR-1998; | 98US-0079294P; |
| PR | 27-MAR-1998; | 98US-0079663P; |
| PR | 27-MAR-1998; | 98US-0079728P; |
| PR | 31-MAR-1998; | 98US-0080165P; |
| PR | 12-JUN-1998; | 98WO-US012456; |
| PR | 14-JUL-1998; | 98WO-US014552; |
| PR | 28-AUG-1998; | 98WO-US017888; |
| PR | 10-SEP-1998; | 98WO-US018824; |
| PR | 14-SEP-1998; | 98WO-US019093; |
| PR | 14-SEP-1998; | 98WO-US019094; |
| PR | 14-SEP-1998; | 98WO-US019177; |
| PR | 16-SEP-1998; | 98WO-US019330; |
| PR | 17-SEP-1998; | 98WO-US019437; |
| PR | 07-OCT-1998; | 98WO-US021141; |
| PR | 29-OCT-1998; | 98WO-US022991; |
| PR | 29-OCT-1998; | 98WO-US022992; |
| PR | 20-NOV-1998; | 98WO-US024855; |
| PR | 01-DEC-1998; | 98WO-US025108; |
| PR | 05-JAN-1999; | 99WO-US000106; |
| PR | 08-MAR-1999; | 99WO-US005028; |
| PR | 10-MAR-1999; | 99WO-US005190; |
| PR | 20-APR-1999; | 99WO-US008615; |
| PR | 14-MAY-1999; | 99WO-US010733; |
| PR | 02-JUN-1999; | 99WO-US012252; |
| PR | 01-SEP-1999; | 99WO-US020111; |
| PR | 08-SEP-1999; | 99WO-US020594; |
| PR | 13-SEP-1999; | 99WO-US020944; |
| PR | 15-SEP-1999; | 99WO-US021090; |
| PR | 15-SEP-1999; | 99WO-US021547; |
| PR | 05-OCT-1999; | 99WO-US023089; |
| PR | 29-NOV-1999; | 99WO-US028214; |
| PR | 30-NOV-1999; | 99WO-US028313; |
| PR | 30-NOV-1999; | 99WO-US028409; |
| PR | 01-DEC-1999; | 99WO-US028301; |
| PR | 01-DEC-1999; | 99WO-US028634; |
| PR | 02-DEC-1999; | 99WO-US028551; |
| PR | 02-DEC-1999; | 99WO-US028564; |
| PR | 02-DEC-1999; | 99WO-US028565; |
| PR | 16-DEC-1999; | 99WO-US030095; |
| PR | 20-DEC-1999; | 99WO-US030911; |
| PR | 20-DEC-1999; | 99WO-US030999; |

30-DEC-1999; 99WO-US031243.
30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US005004.
01-MAR-2000; 2000WO-US005601.
02-MAR-2000; 2000WO-US005746.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-352836/33.
DR N-PSDB; ACA67086.
XX
PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
PS Claim 12; Fig 186; 643pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ABU80870-ABU81144 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdsIDEntry.html
XX
SQ Sequence 364 AA;

RESULT 9
ABU66662
ID ABU66662 standard; protein; 364 AA.
XX
AC ABU66662;
XX
DT 23-MAY-2003 (first entry)
XX
DE Human PRO polypeptide #93.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-00143114.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-332040/31.
N-PSDB; ACA03695.

New secreted and transmembrane PRO nucleic acids, useful for gene
therapy, in chromosome and gene mapping, as chromosome markers, in tissue
typing, and in chromosome identification.

Claim 12; Fig 186; 660pp; English.

The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are useful for detecting other PRO polypeptides, for linking
bioactive molecules to cells expressing PRO polypeptides, and for
biological activities of cells expressing PRO polypeptides, and for
identifying agonists or antagonists. The PRO polypeptides are useful for

CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the
CC human PRO polypeptides of the invention. Note: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipSIDEntry.html
XX
SQ Sequence 364 AA;

Query Match 100.0%; Score 1742; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRDETIQKNGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db |||||||
43 LYRDETIQKNGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 102
QY 61 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db |||||||
103 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDFOPAAASETNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 180
Db |||||||
163 LLEDFOPAAASETNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 222
QY 181 PESWQEDLENMYLDTPIYRGRSYHDKRKSVDLRLNDDAKRYSCTPRNYSVNIREEELKLA 240
Db |||||||
223 PESWQEDLENMYLDTPIYRGRSYHDKRKSVDLRLNDDAKRYSCTPRNYSVNIREEELKLA 282
QY 241 NVVFFPRCLLVQRCGNCGGTVNWRSCNCGTKVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db |||||||
283 NVVFFPRCLLVQRCGNCGGTVNWRSCNCGTKVKKYHEVLQFEPGHIKRRGRAKTMA 342
QY 301 LVDIQLDHERCDCICSSRPPR 322
Db |||||||
343 LVDIQLDHERCDCICSSRPPR 364

RESULT 10
ABU59743
ID ABU59743 standard; protein; 364-AA.
XX
AC ABU59743;
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO4345.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-00140808.
XX
PR 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 99WO-US031274.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.

PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.

PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-466355/44.
DR N-PSDB; ACD41887.

PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
PT PRO4978, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.

XX Claim 12; Fig 186; 659pp; English.

CC The invention relates to an isolated nucleic acid comprising at least 80%
CC sequence identity to a PRO (secreted and transmembrane protein) cDNA
CC comprising a nucleic acid (a) encoding a PRO polypeptide, or its
CC extracellular domain (with or without its associated signal peptide),
CC which comprises any of the 275 120-850 residue amino acid sequences,
CC given in the specification; (b) comprising any of the 275 300-3500
CC nucleotide sequences, given in the specification; or (c) comprising the
CC full-length coding sequence of the nucleotide sequences given in the
CC specification, or of the DNA deposited under any of the American Type
CC Culture Collection (ATCC) Accession Numbers listed in the specification.
CC Also included are a vector comprising the novel nucleic acid, a host cell
CC comprising the vector, producing a PRO polypeptide, the isolated PRO
CC polypeptides detailed above, a chimeric molecule comprising the PRO
CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, detecting a PRO polypeptide in a sample suspected of containing
CC the PRO polypeptide, linking a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulating at least one biological activity of a cell
CC expressing a PRO polypeptide, stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
CC cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
CC modulating the uptake of glucose or FFA by skeletal muscle cells or
CC adipocyte cells, stimulating the proliferation or differentiation of
CC chondrocyte cells (or proliferation of or gene expression in pericyte
CC cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
CC binding of A-peptide to factor VIIa, or differentiation of adipocyte
CC cells, detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences given
CC in the specification. The polynucleotide is useful in molecular biology,
CC including uses as hybridisation probes, in chromosome and gene mapping,
CC in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide may also be used in preparing PRO polypeptides by
CC recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptide or the
CC antibody is used in preparing a medicament for treating a condition
CC responsive to the polypeptide or antibody, such as tumours, and in
CC various diagnostic assays. The present sequence represents a PRO
XX polypeptide

SQ Sequence 364 AA;

Query Match 100.0%; Score 1742; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRDETIQKNGYVQSPRFNSYPRNLLLTWRLHSQENTRIQLVFDNQGLEEAENDI 60
Db 43 LYRDETIQKNGYVQSPRFNSYPRNLLLTWRLHSQENTRIQLVFDNQGLEEAENDI 102

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W; Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-331925/31.

N-PSDB; ACA04116.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer.

Claim 12; Fig 186; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor alpha) from human blood, (and the proliferation of differentiation of chondrocyte cells, the proliferation of, or gene expression in pericyte cells, the release or proteoglycans from cartilage, proliferation of inner ear urticular supporting cells, the proliferation of T-lymphocyte cells, the release of a cytokine from peripheral blood mononuclear cells (PBMC), or the proliferation of endothelial cells), a method for modulating the uptake of glucose or free fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the binding of A-peptide to factor VIIA, or the differentiation of adipocyte cells, a method for detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences cited above. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a PRO protein of the invention

Sequence 364 AA;

| | | | | |
|-----------------------|-----------------|------------------|-----------|-------------|
| Query Match | 100.0%; | Score 1742; | DB 6; | Length 364; |
| Best Local Similarity | 100.0%; | Pred. No.5e-166; | | |
| Matches 322; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|--|-----|
| Qy | 1 | LYRRDETIQKNGVGVQSPRPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI | 60 |
| Db | 43 | LYRRDETIQKNGVGVQSPRPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI | 102 |
| Qy | 61 | CRYDFVEVEDISETSTIIRGRWCGHKEVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS | 120 |
| Db | 103 | CRYDFVEVEDISETSTIIRGRWCGHKEVPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS | 162 |
| Qy | 121 | LLEDFFQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN | 180 |
| Db | 163 | LLEDFFQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN | 222 |
| Qy | 181 | PESWQEDLENMYLDTPRYGRGRSYHDRKSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA | 240 |
| Db | 223 | PESWQEDLENMYLDTPRYGRGRSYHDRKSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA | 282 |
| Qy | 241 | NVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA | 300 |
| Db | 283 | NVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA | 342 |

| | | | |
|-----------|---|--------------------------|-----|
| QY | 301 | LVDIQLDHHHERCDCICSSRRPPR | 322 |
| | | | |
| Db | 343 | LVDIQLDHHHERCDCICSSRRPPR | 364 |
| RESULT 13 | | | |
| ID | ADA45705 | | |
| AC | ADA45705 standard; protein; 364 AA. | | |
| XX | ADA45705; | | |
| XX | AC | | |
| XX | DT | | |
| XX | 20-NOV-2003 | (first entry) | |
| DE | Novel human secreted and transmembrane protein PRO4345. | | |
| XX | XX | | |
| KW | Human; secreted and transmembrane protein; PRO; | | |
| KW | Tumour necrosis factor alpha release; TNF-alpha release; | | |
| KW | glucose uptake modulator; FFA uptake modulator; | | |
| KW | cell proliferation stimulator; cell differentiation stimulator; | | |
| KW | cell differentiation inhibitor; cytokine release stimulator; tumour; | | |
| KW | lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; | | |
| KW | cervical tumour; liver tumour; chromosome mapping; gene mapping; | | |
| KW | gene therapy; chromosome identification; chromosome marker. | | |
| XX | XX | | |
| OS | Homo sapiens. | | |
| XX | XX | | |
| PN | US2003022328-A1. | | |
| XX | XX | | |
| PD | 30-JAN-2003. | | |
| XX | XX | | |
| PF | 16-APR-2002; 2002US-00123904. | | |
| XX | XX | | |
| PR | 31-MAR-1997; 97WO-US005230. | | |
| PR | 12-JUN-1998; 98WO-US012456. | | |
| PR | 14-JUL-1998; 98WO-US014552. | | |
| PR | 28-AUG-1998; 98WO-US017888. | | |
| PR | 10-SEP-1998; 98WO-US018824. | | |
| PR | 14-SEP-1998; 98WO-US019093. | | |
| PR | 14-SEP-1998; 98WO-US019094. | | |
| PR | 14-SEP-1998; 98WO-US019177. | | |
| PR | 16-SEP-1998; 98WO-US019330. | | |
| PR | 17-SEP-1998; 98WO-US019437. | | |
| PR | 07-OCT-1998; 98WO-US021141. | | |
| PR | 29-OCT-1998; 98WO-US022991. | | |
| PR | 29-OCT-1998; 98WO-US022992. | | |
| PR | 20-NOV-1998; 98WO-US024855. | | |
| PR | 01-DEC-1998; 98WO-US025108. | | |
| PR | 05-JAN-1999; 99WO-US000106. | | |
| PR | 08-MAR-1999; 99WO-US005028. | | |
| PR | 10-MAR-1999; 99WO-US005190. | | |
| PR | 20-APR-1999; 99WO-US008615. | | |
| PR | 14-MAY-1999; 99WO-US010733. | | |
| PR | 02-JUN-1999; 99WO-US012252. | | |
| PR | 01-SEP-1999; 99WO-US020111. | | |
| PR | 08-SEP-1999; 99WO-US020594. | | |
| PR | 13-SEP-1999; 99WO-US020944. | | |
| PR | 15-SEP-1999; 99WO-US021090. | | |
| PR | 15-SEP-1999; 99WO-US021547. | | |
| PR | 05-OCT-1999; 99WO-US023089. | | |
| PR | 29-NOV-1999; 99WO-US028214. | | |
| PR | 30-NOV-1999; 99WO-US028313. | | |
| PR | 30-NOV-1999; 99WO-US028409. | | |
| PR | 01-DEC-1999; 99WO-US028301. | | |
| PR | 01-DEC-1999; 99WO-US028634. | | |
| PR | 02-DEC-1999; 99WO-US028551. | | |
| PR | 02-DEC-1999; 99WO-US028564. | | |
| PR | 02-DEC-1999; 99WO-US028565. | | |
| PR | 16-DEC-1999; 99WO-US030095. | | |
| PR | 20-DEC-1999; 99WO-US030911. | | |
| PR | 20-DEC-1999; 99WO-US030999. | | |
| PR | 22-DEC-1999; 99WO-US030720. | | |
| PR | 30-DEC-1999; 99WO-US031243. | | |
| PR | 30-DEC-1999; 99WO-US031274. | | |

PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-584997/55.
DR N-PSDB; ADA45704.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 12; Fig 186; 659pp; English.

XX The invention describes 305 nucleic acids encoding PRO (secreted and
CC transmembrane) polypeptides (I). (I) is useful for stimulating the
CC release of TNF-alpha from human blood, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating the proliferation or differentiation of chondrocyte cells,
CC for stimulating the proliferation of or gene expression in pericyte
CC cells, for stimulating the release of proteoglycans from cartilage, for
CC stimulating the proliferation of inner ear utricular supporting cells,
CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
CC the release of a cytokine from PBMC cells, for inhibiting the binding of
CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
CC cells, for stimulating proliferation of endothelial cells, for detecting
CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
CC are useful for isolating genomic and cDNA nucleotide sequences or
CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
CC in assays to identify other proteins or molecules involved in binding
CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
CC and gene mapping, in generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptide, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, in gene therapy, for
CC chromosome identification, as chromosome marker, and for generating
CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
CC detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. (I) and (II) are useful for tissue typing. This is the amino
CC acid sequence of a novel human secreted and transmembrane PRO
CC polypeptide.
XX
SQ Sequence 364 AA;

Query Match 100.0%; Score 1742; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LYRDETIQVKGNGYVQSPRFPNSYPRLNLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db |||||
QY 61 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db |||||
QY 103 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDQFPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN 180
Db |||||
QY 163 LLEDQFPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRGRSYHDKSKVLDRLNDDAKRYSCTPRNSVNIREEKLKLA 240
Db |||||
QY 223 PESWQEDLENMYLDTPRYGRGRSYHDKSKVLDRLNDDAKRYSCTPRNSVNIREEKLKLA 282
QY 241 NVVFFPRCLLVQRCGGNCGGTVNWRSCITNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db |||||
QY 283 NVVFFPRCLLVQRCGGNCGGTVNWRSCITNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 342
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db |||||
QY 343 LVDIQLDHHERCDCICSSRPPR 364

RESULT 14
ADA76136
ID ADA76136 standard; protein; 364 AA.

XX ADA76136;
XX
DT 20-NOV-2003 (first entry)
XX Human PRO polypeptide #93.
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;

KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW liver; microvascular endothelial cell; glucose; FFA;
KW skeletal muscle cell; adipocyte cell; pericyte cell;
KW inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell tube formation; bone disorder; cartilage disorder;
KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
KW immune system cell infiltration.

XX Homo sapiens.

XX US2003073212-A1.

PN 17-APR-2003.

PD 16-APR-2002; 2002US-00123903.

XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00860216.
PR 18-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-687639/65.

N-PSDB; ADA76135.

New isolated nucleic acid encoding a secreted and transmembrane polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 12; Fig 186; 659pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are

CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC proliferation of or gene expression in pericyte cells, for stimulating
CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent is also available in electronic format from
CC USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 364 AA;

Query Match 100.0%; Score 1742; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRRDETIQKNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQGLEEAENDI 60
Db |||||
QY 43 LYRRDETIQKNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQGLEEAENDI 102
Db |||||
QY 61 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db |||||
QY 103 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 162
Db |||||
QY 121 LLEDFPQAAASETNWESVTSSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKYFN 180
Db |||||
QY 163 LLEDFPQAAASETNWESVTSSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKYFN 222
Db |||||
QY 181 PESWQEDLENMYLDTFPRYGRSYHDKRSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA 240
Db |||||
QY 223 PESWQEDLENMYLDTFPRYGRSYHDKRSKVDLRLNDDAKRYSCTPRNYSVNIREELKLA 282
Db |||||
QY 241 NVVFFPRCLLVQRCGNGCGGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db |||||
QY 283 NVVFFPRCLLVQRCGNGCGGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 342
Db |||||
QY 301 LVDIQLDHERCDCICSSRPPR 322
Db |||||
QY 343 LVDIQLDHERCDCICSSRPPR 364
Db |||||

RESULT 15
ADA18786
ID ADA18786 standard; protein; 364 AA.
XX
AC ADA18786;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human PRO polypeptide #93.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;
KW colon; breast; prostate; rectum; cervix; liver; tumour; cancer;
KW glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;
KW cartilage; inner ear utricular supporting cell; cytokine; A-peptide;
KW factor VIIA; endothelial cell.
XX
OS Homo sapiens.
XX
PN US2003054517-A1.
XX

PD 20-MAR-2003.
XX
PF 08-MAY-2002; 2002US-00141755.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-521854/49.
DR N-PSDB; ADA18785.
XX
PT New PRO nucleic acid, useful for preparing a composition for treating
PT e.g., tumors.
XX
PS Claim 12; Fig 186; 660pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, cervical and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for modulating the uptake of glucose or FFA by adipocyte
CC cells, for stimulating the proliferation of or gene expression in
CC pericyte cells, for stimulating the release of proteoglycans from
CC cartilage, for stimulating the proliferation of inner ear utricular
CC supporting cells, for stimulating the release of cytokines from PBMC
CC cells, for inhibiting the binding of A-peptide to factor VIIA, for
CC inhibiting the differentiation of adipocyte cells and for stimulating the
CC proliferation of endothelial cells. This sequence represents a human PRO
CC polypeptide of the invention. Note: The sequence data for this patent is
CC also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX

| | | | | | | | | | | |
|----|-----------------------|---|------------------|-----------|-------------|--|--|--|--|--|
| SQ | Sequence 364 AA; | | | | | | | | | |
| | Query Match | 100.0%; | Score 1742; | DB 6; | Length 364; | | | | | |
| | Best Local Similarity | 100.0%; | Pred. No.5e-166; | | | | | | | |
| | Matches 322; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; | | | | | |
| QY | 1 | LYRRDETIQVKGNGYVQSPRFNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI | 60 | | | | | | | |
| Db | 43 | LYRRDETIQVKGNGYVQSPRFNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI | 102 | | | | | | | |
| QY | 61 | CRYDFVEVEDISETSTIIRGRWCCHKVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS | 120 | | | | | | | |
| Db | 103 | CRYDFVEVEDISETSTIIRGRWCCHKVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS | 162 | | | | | | | |
| QY | 121 | LLEDQFAAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKIAEFTVEDLLKYFN | 180 | | | | | | | |
| Db | 163 | LLEDQFAAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKIAEFTVEDLLKYFN | 222 | | | | | | | |
| QY | 181 | PESWQEDLENMYLDTPRYGRSYHDKRSKVDLDRLNDDAKRYCTPRNYSVNIREELKLA | 240 | | | | | | | |
| Db | 223 | PESWQEDLENMYLDTPRYGRSYHDKRSKVDLDRLNDDAKRYCTPRNYSVNIREELKLA | 282 | | | | | | | |
| QY | 241 | NVVFPRCLLVQRCGNGCGGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA | 300 | | | | | | | |
| Db | 283 | NVVFPRCLLVQRCGNGCGGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA | 342 | | | | | | | |
| QY | 301 | LVDIQLDHHERCDCICSSRPPR | 322 | | | | | | | |
| Db | 343 | LVDIQLDHHERCDCICSSRPPR | 364 | | | | | | | |

Search completed: October 29, 2004, 23:29:11
Job time : 164 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2004, 23:24:15 ; Search time 39 Seconds
(without alignments)
547.549 Million cell updates/sec

Title: US-10-086-623-6
Perfect score: 1742
Sequence: 1 LYRRDETIQKNGYVQSPR.....DIQLDHERCDCICSSRPPR 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------|
| 1 | 1742 | 100.0 | 322 | 4 | US-09-438-046-6 |
| 2 | 1742 | 100.0 | 364 | 4 | US-10-140-002-186 |
| 3 | 1742 | 100.0 | 370 | 4 | US-09-457-066-37 |
| 4 | 1742 | 100.0 | 370 | 4 | US-09-540-224-2 |
| 5 | 1742 | 100.0 | 370 | 4 | US-09-564-595D-2 |
| 6 | 1742 | 100.0 | 370 | 4 | US-09-706-968-37 |
| 7 | 1742 | 100.0 | 370 | 4 | US-09-808-972-2 |
| 8 | 1742 | 100.0 | 370 | 4 | US-09-823-033-5 |
| 9 | 1742 | 100.0 | 370 | 4 | US-09-438-046-8 |
| 10 | 1561 | 89.6 | 370 | 4 | US-09-540-224-4 |
| 11 | 1561 | 89.6 | 370 | 4 | US-09-564-595D-53 |
| 12 | 1561 | 89.6 | 370 | 4 | US-09-808-972-4 |
| 13 | 1403 | 80.5 | 317 | 4 | US-09-564-595D-56 |
| 14 | 1357.5 | 77.9 | 316 | 4 | US-09-564-595D-55 |
| 15 | 1095 | 62.9 | 303 | 4 | US-09-564-595D-57 |
| 16 | 1061.5 | 60.9 | 302 | 4 | US-09-564-595D-54 |
| 17 | 982 | 56.4 | 200 | 4 | US-09-438-046-4 |
| 18 | 750.5 | 43.1 | 345 | 4 | US-09-457-066-43 |
| 19 | 750.5 | 43.1 | 345 | 4 | US-09-564-595D-35 |
| 20 | 750.5 | 43.1 | 345 | 4 | US-09-706-968-43 |
| 21 | 750.5 | 43.1 | 345 | 4 | US-09-823-033-4 |
| 22 | 739.5 | 42.5 | 323 | 4 | US-09-468-647-1 |
| 23 | 739.5 | 42.5 | 345 | 3 | US-09-040-220D-2 |
| 24 | 739.5 | 42.5 | 345 | 4 | US-09-457-066-2 |
| 25 | 739.5 | 42.5 | 345 | 4 | US-09-265-686-2 |
| 26 | 739.5 | 42.5 | 345 | 4 | US-09-540-224-5 |
| 27 | 739.5 | 42.5 | 345 | 4 | US-09-564-595D-33 |

| | | | | | | |
|----|-------|------|------|---|-------------------|-------------------|
| 28 | 739.5 | 42.5 | 345 | 4 | US-09-706-968-2 | Sequence 2, Appli |
| 29 | 739.5 | 42.5 | 345 | 4 | US-09-723-749-2 | Sequence 2, Appli |
| 30 | 739.5 | 42.5 | 345 | 4 | US-09-823-033-2 | Sequence 2, Appli |
| 31 | 739.5 | 42.5 | 345 | 4 | US-10-140-002-286 | Sequence 286, App |
| 32 | 739.5 | 42.5 | 345 | 4 | US-09-468-647-2 | Sequence 2, Appli |
| 33 | 651 | 37.4 | 121 | 4 | US-09-438-046-18 | Sequence 18, Appl |
| 34 | 637 | 36.6 | 119 | 4 | US-09-438-046-19 | Sequence 19, Appl |
| 35 | 380 | 21.8 | 66 | 4 | US-09-438-046-2 | Sequence 2, Appli |
| 36 | 329.5 | 18.9 | 132 | 4 | US-09-468-647-29 | Sequence 29, Appl |
| 37 | 328.5 | 18.9 | 168 | 4 | US-09-468-647-27 | Sequence 27, Appl |
| 38 | 295.5 | 17.0 | 111 | 4 | US-09-468-647-26 | Sequence 26, Appl |
| 39 | 187.5 | 10.8 | 788 | 1 | US-08-572-225-1 | Sequence 1, Appli |
| 40 | 187.5 | 10.8 | 986 | 4 | US-09-285-385C-19 | Sequence 19, Appl |
| 41 | 186.5 | 10.7 | 730 | 3 | US-08-872-757-2 | Sequence 2, Appli |
| 42 | 186.5 | 10.7 | 730 | 4 | US-09-850-048A-2 | Sequence 2, Appli |
| 43 | 186.5 | 10.7 | 1015 | 4 | US-09-285-385C-2 | Sequence 2, Appli |
| 44 | 183.5 | 10.5 | 1012 | 4 | US-09-285-385C-4 | Sequence 4, Appli |
| 45 | 180.5 | 10.4 | 101 | 3 | US-09-374-135-6 | Sequence 6, Appli |

ALIGNMENTS

RESULT 1
US-09-438-046-6
; Sequence 6, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-6

Query Match 100.0%; Score 1742; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.4e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| QY | 1 | LYRRDETIQKNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEANDI | 60 |
| Db | 1 | LYRRDETIQKNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEANDI | 60 |
| QY | 61 | CRYDFVEVEDISETSTIIRGRWCWGHEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS | 120 |
| Db | 61 | CRYDFVEVEDISETSTIIRGRWCWGHEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS | 120 |
| QY | 121 | LLEDFOPAASSETNWESVTSSISGVSYNSPSTPTLIADALDKIAEFTVEDLLKYFN | 180 |

Db 121 LLEDQPAAASETNWESVTSSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKYFN 180
QY 181 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLDRLNDDAKRYSC TPRNYSVNIREELKLA 240
Db 181 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLDRLNDDAKRYSC TPRNYSVNIREELKLA 240
QY 241 NVVFFPRCLLVQRCGNGCGGTVNWRSC TNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 241 NVVFFPRCLLVQRCGNGCGGTVNWRSC TNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db 301 LVDIQLDHHERCDCICSSRPPR 322

RESULT 2

US-10-140-002-186
; Sequence 186, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maurea
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 186
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-002-186

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Best Local Similarity 100.0%; Pred. No. 1.7e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 43 LYRDETIQVKGNGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 102
QY 61 CRYDFVEVEDISETSTIIRGRWCGRHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 120
Db 103 CRYDFVEVEDISETSTIIRGRWCGRHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDQPAAASETNWESVTSSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKYFN 180
Db 163 LLEDQPAAASETNWESVTSSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLDRLNDDAKRYSC TPRNYSVNIREELKLA 240
Db 223 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLDRLNDDAKRYSC TPRNYSVNIREELKLA 282
QY 241 NVVFFPRCLLVQRCGNGCGGTVNWRSC TNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 283 NVVFFPRCLLVQRCGNGCGGTVNWRSC TNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 342

QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db 343 LVDIQLDHHERCDCICSSRPPR 364
RESULT 3
US-09-457-066-37
; Sequence 37, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-37
Query Match 100.0%; Score 1742; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LYRDETIQVKGNGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db 49 LYRDETIQVKGNGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 108
QY 61 CRYDFVEVEDISETSTIIRGRWCGRHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 120
Db 109 CRYDFVEVEDISETSTIIRGRWCGRHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYS 168
QY 121 LLEDQPAAASETNWESVTSSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKYFN 180
Db 169 LLEDQPAAASETNWESVTSSISGVSYNPSVTDPTLIADALDKKIAEFTVEDLLKYFN 228
QY 181 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLDRLNDDAKRYSC TPRNYSVNIREELKLA 240
Db 229 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLDRLNDDAKRYSC TPRNYSVNIREELKLA 283
QY 241 NVVFFPRCLLVQRCGNGCGGTVNWRSC TNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 289 NVVFFPRCLLVQRCGNGCGGTVNWRSC TNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db 349 LVDIQLDHHERCDCICSSRPPR 370

RESULT 4

US-09-540-224-2
; Sequence 2, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04

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; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-2

Query Match      100.0%; Score 1742; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db 109 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 168

QY 121 LLEDFOPAASETNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 180
Db 169 LLEDFOPAASETNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 228

QY 181 PESWQEDLENMYLDTPRYGRGRSYHDKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 240
Db 229 PESWQEDLENMYLDTPRYGRGRSYHDKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 288

QY 241 NVVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 289 NVVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348

QY 301 LVDIQLDHERCDCICSSRPPR 322
Db 349 LVDIQLDHERCDCICSSRPPR 370

RESULT 5
US-09-564-595D-2
; Sequence 2, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-595D-2

Query Match      100.0%; Score 1742; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 49 LYRRDETIQVKGNGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDI 108

QY 61 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120

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Db 109 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 168

QY 121 LLEDFOPAASETNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 180
Db 169 LLEDFOPAASETNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 228

QY 181 PESWQEDLENMYLDTPRYGRGRSYHDKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 240
Db 229 PESWQEDLENMYLDTPRYGRGRSYHDKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 288

QY 241 NVVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 289 NVVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348

QY 301 LVDIQLDHERCDCICSSRPPR 322
Db 349 LVDIQLDHERCDCICSSRPPR 370

RESULT 6
US-09-706-968-37
; Sequence 37, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-706-968-37

Query Match      100.0%; Score 1742; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRRDETIQVKGNGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDI 60
Db 49 LYRRDETIQVKGNGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDI 108

QY 61 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db 109 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 168

QY 121 LLEDFOPAASETNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 180
Db 169 LLEDFOPAASETNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 228

QY 181 PESWQEDLENMYLDTPRYGRGRSYHDKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 240
Db 229 PESWQEDLENMYLDTPRYGRGRSYHDKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 288

QY 241 NVVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 289 NVVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348

QY 301 LVDIQLDHERCDCICSSRPPR 322
Db 349 LVDIQLDHERCDCICSSRPPR 370

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RESULT 7
US-09-808-972-2
; Sequence 2, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-972-2

Query Match 100.0%; Score 1742; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
49 LYRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 108
QY 61 CRYDFVEVEDISSETIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
109 CRYDFVEVEDISSETIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 168
QY 121 LLEDQPAAASETNWESVTSSISGVSYNDRKSKVDLRLNDDAKRYSCPTPNYSVNIREELKLA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
169 LLEDQPAAASETNWESVTSSISGVSYNDRKSKVDLRLNDDAKRYSCPTPNYSVNIREELKLA 228
QY 181 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLRLNDDAKRYSCPTPNYSVNIREELKLA 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
229 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLRLNDDAKRYSCPTPNYSVNIREELKLA 288
QY 241 NVVFFPRCLLVQRCGNGCGCTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
289 NVVFFPRCLLVQRCGNGCGCTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
349 LVDIQLDHHERCDCICSSRPPR 370

RESULT 8
US-09-823-033-5
; Sequence 5, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-5

Query Match 100.0%; Score 1742; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
49 LYRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 108
QY 61 CRYDFVEVEDISSETIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
109 CRYDFVEVEDISSETIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 168
QY 121 LLEDQPAAASETNWESVTSSISGVSYNDRKSKVDLRLNDDAKRYSCPTPNYSVNIREELKLA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
169 LLEDQPAAASETNWESVTSSISGVSYNDRKSKVDLRLNDDAKRYSCPTPNYSVNIREELKLA 228
QY 181 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLRLNDDAKRYSCPTPNYSVNIREELKLA 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
229 PESWQEDLENMYLDTPRYGRSYHDRKSKVDLRLNDDAKRYSCPTPNYSVNIREELKLA 288
QY 241 NVVFFPRCLLVQRCGNGCGCTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
289 NVVFFPRCLLVQRCGNGCGCTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
349 LVDIQLDHHERCDCICSSRPPR 370

RESULT 9
US-09-438-046-8
; Sequence 8, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-8


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; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0.
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-808-972-4

Query Match      89.6%; Score 1561; DB 4; Length 370;
Best Local Similarity 86.6%; Pred. No. 1.2e-153;
Matches 279; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 1 LYRDETIQKNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEANDI 60
Db 49 LYQREENIQVTSNGHVQSPRFPNSYPRNLLLTWRLSQEKTRIQLSFDHQFGLAEANDI 108

QY 61 CRYDFEVEDISETSTIIRGRWCCHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
Db 109 CRYDFEVEEVSESTIVRGRWCCHKEIPPRITSRTNQIKITFKSDDYFVAKPGFKIYYS 168

QY 121 LLEDFOAAAASETNWESVTSSISGVSYNSPSVTDTLADALDKKIAEFDTVEDLLKYFN 180
Db 169 FVEDFOPEAAASETNWESVTSSFSGVSYHSPSITDTLTADALDKTVAEFDTVEDLLKHFN 228

QY 181 PESWQEDLENMYLDTPRYGRGRSYHDKSKVDLDRNDDAKRYSCTPRNYSVNIREELKLA 240
Db 229 PVSWQDDLENLYLDTPHYRGRGRSYHDKSKVDLDRNDVDVKRYSCTPRNHVSNLRREELKLT 288

QY 241 NVVFFPRCLLVQRCGNCGGCTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 289 NAVFFPRCLLVQRCGNCGGCTVNWKSCTCSGKTVKKYHEVLKFEPGHFRGKAKNMA 348

QY 301 LVDIQLDHERCDCICSSRPPR 322
Db 349 LVDIQLDHERCDCICSSRPPR 370

RESULT 13
US-09-564-595D-56
; Sequence 56, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

Query Match      77.9%; Score 1357.5; DB 4; Length 316;
Best Local Similarity 80.0%; Pred. No. 1.3e-132;
Matches 256; Conservative 24; Mismatches 33; Indels 7; Gaps 4;

QY 5 DETIQKNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLAEANDICRY 63
Db 2 ERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAEENVWIQLTFDERFGLDEPDDICKY 61

QY 64 DFVEVEDISETSTIIRGRWCCHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS-L 122
Db 62 DFVEVEEPSDGT--ILGRWCSGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVM 119
```

```
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-56

Query Match      80.5%; Score 1403; DB 4; Length 317;
Best Local Similarity 83.8%; Pred. No. 2.5e-137;
Matches 263; Conservative 14; Mismatches 33; Indels 4; Gaps 2;

QY 4 RDETIQKNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRY 63
Db 1 RDETIQKNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEANDICRY 60

QY 64 DFVEVEDISETSTIIRGRWCCHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLE 123
Db 61 DFVEVEDISETSTIIRGRWCCHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLE 120

QY 124 DFQPAASSETNWESVTSSISGVSYNSPSVTDTLADALDKKIAEFDTVEDLLKYFNPS 183
Db 121 DFQPAASSETNWESVTSSISGVSYNSPSVTDTLADALDKKIAEFDTVEDLLKYFNPS 180

QY 184 WQEDLENMYLDTPRYGRGRSYHDKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELKLANV 242
Db 181 WQEDLENMYLDTPRYGRGRSYHDKSKVVDLNLNLTTEEVRLYSCTPRNFVSIREELKRTDT 240

QY 243 VFFPRCLLVQRCGNCGGCTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMAV 302
Db 241 IFWPGCLLVKRCGNCACCLHNCQCQVPSKVTKKYHEVLQLRP---KTGVRGLHKSLT 297

QY 303 DIQLDHERCDCIC 316
Db 298 DVALEHHEECDCVC 311

RESULT 14
US-09-564-595D-55
; Sequence 55, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

Query Match      77.9%; Score 1357.5; DB 4; Length 316;
Best Local Similarity 80.0%; Pred. No. 1.3e-132;
Matches 256; Conservative 24; Mismatches 33; Indels 7; Gaps 4;

QY 5 DETIQKNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLAEANDICRY 63
Db 2 ERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAEENVWIQLTFDERFGLDEPDDICKY 61

QY 64 DFVEVEDISETSTIIRGRWCCHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS-L 122
Db 62 DFVEVEEPSDGT--ILGRWCSGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVM 119
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Search completed: October 29, 2004, 23:33:57
Job time : 40 secs

| | | | |
|----|-----|---|-----|
| Qy | 123 | EDFQAAAASETNWESVTSSISGVSYNSPSPVTDPTLIADALDKKIAEFDTVEDLLKYFNPE | 182 |
| Db | 120 | PQFTEA---ETNWESVTSSISGVSYNSPSPVTDPTLIADALDKKIAEFDTVEDLLKYFNPE | 176 |
| Qy | 183 | SWQEDLENMYLDTPRYGRGRSYHDKRSKVDLDRLNDDAKRYSCTPRNTSVNIREELKLANV | 242 |
| Db | 177 | SWQEDLENMYLDTPRYGRGRSYHDKRSKVDLDRLNDDAKRYSCTPRNTSVNIREELKLANV | 236 |
| Qy | 243 | VFFPRCLLVQRCGGNCGCGTVNWRSGTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALV | 302 |
| Db | 237 | VFFPRCLLVQRCGGNCGCGTVNWRSGTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALV | 296 |
| Qy | 303 | DIQLDHHERCDCICSSRPPR | 322 |
| Db | 297 | DIQLDHHERCDCICSSRPPR | 316 |

RESULT 15

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US-09-564-595D-57
; Sequence 57, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-57

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| | | | | |
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| Query Match | 62.9%; | Score 1095; | DB 4; | Length 303; |
| Best Local Similarity | 67.4%; | Pred. No. 2.5e-105; | | |
| Matches 213; | Conservative | 26; | Mismatches 55; | Indels 22; |
| | | | | Gaps 5; |

| | | | |
|----|-----|---|-----|
| QY | 4 | RDETIQVKNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRY | 63 |
| Db | 1 | RDETIQVKNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRY | 60 |
| QY | 64 | DFVEVEDISETSTIIIRGRWCGHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLE | 123 |
| Db | 61 | DFVEVEDISETSTIIIRGRWCGHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLE | 120 |
| QY | 124 | DFQPAASSETNWESVTSSISGVSYNSPSVTDPT-LIADALDKKIAEFDTVEDLLKYFNPE | 182 |
| Db | 121 | DFQPAASV-----SPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPE | 164 |
| QY | 183 | SWQEDLENMYLDTPRYGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELKLA | 240 |
| Db | 165 | RWQLDLEDLYRPTWQLLGKAFVGRKSRVVDNLLTTEEVRLYSCTPRNFSVSIREECLKRT | 224 |
| QY | 241 | NVVFPRCLLVQRCGGNCGGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA | 300 |
| Db | 225 | DTIFWEGCLLVKRCGGNACCLHNCNECQCVP SKVTKKYHEVLQLRP---KTGVRGLHKS | 281 |
| QY | 301 | LVDIQLDHHERCDCIC | 316 |
| Db | 282 | LTDVALEHHEECDVC | 297 |

C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted
F;130-321/Domain: astacin homology <AST>
F;322-431/Domain: C1r/C1s repeat homology <C1R1>
F;435-544/Domain: C1r/C1s repeat homology <C1R2>
F;551-587/Domain: EGF homology <EG1>
F;591-700/Domain: C1r/C1s repeat homology <C1R3>
F;707-742/Domain: EGF homology <EG2>
F;747-856/Domain: C1r/C1s repeat homology <C1R4>
F;860-973/Domain: C1r/C1s repeat homology <C1R5>
F;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F;213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F;214/Active site: Glu #status predicted
F;565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 10.8%; Score 187.5; DB 1; Length 986;
Best Local Similarity 39.4%; Pred. No. 1.9e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

QY 11 KNGYVQSPRFPNSYPRLNLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVED 70
Db 597 KLNGSITSPGWPKEYPNKNCTIQLVAPTQYRISLQFD---FFETEGNDVCKYDFVEVRS 653

QY 71 ISETSTIIRGRWCCHKKEVPPIKSRNTQIKITFKSDDYFVAKPGFKIYY 119
Db 654 GLTADSKLHGKFCG-SEKPEVITSQYNNMRVEFKSDN-TVSKKGFKAHF 700

RESULT 8
I49540
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49540
R;Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A;Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
A;Reference number: I49540; MUID:94229342; PMID:8174772
A;Accession: I49540
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-991 <RES>
A;Cross-references: UNIPROT:P98063; GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607
C;Genetics:
A;Gene: Bmp-1
C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C;Keywords: hydrolase; metalloproteinase; zinc
F;135-326/Domain: astacin homology <AST>
F;556-592/Domain: EGF homology <EG1>
F;596-705/Domain: C1r/C1s repeat homology <C1R>
F;712-747/Domain: EGF homology <EG2>
F;218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
F;219/Active site: Glu #status predicted

Query Match 10.8%; Score 187.5; DB 2; Length 991;
Best Local Similarity 39.4%; Pred. No. 1.9e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

QY 11 KNGYVQSPRFPNSYPRLNLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVED 70
Db 602 KLNGSITSPGWPKEYPNKNCTIQLVAPTQYRISLQFD---FFETEGNDVCKYDFVEVRS 658

QY 71 ISETSTIIRGRWCCHKKEVPPIKSRNTQIKITFKSDDYFVAKPGFKIYY 119
Db 659 GLTADSKLHGKFCG-SEKPEVITSQYNNMRVEFKSDN-TVSKKGFKAHF 705

RESULT 9
T09456
intrinsic factor-B12 receptor Cubilin precursor - human
C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
ion.
A;Reference number: Z16677; MUID:98241400; PMID:9572993
A;Accession: T09456
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3623 <KOZ>
A;Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g39
C;Genetics:
A;Map position: 10p12
C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C;Keywords: receptor; vitamin B12 uptake
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F;436-467/Domain: EGF homology <EGF>

Query Match 10.6%; Score 184.5; DB 2; Length 3623;
Best Local Similarity 24.3%; Pred. No. 1.7e-05;
Matches 85; Conservative 34; Mismatches 120; Indels 111; Gaps 17;

QY 8 IQVKGNGYVQSPRFPNSYPRLNLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVE 67
Db 935 ILTESTGTIQSPGHPNVYPHGINCTWHILVQPNHLIHLMFET-FHLEFHYN--CTNDYLE 991

QY 68 VEDI-SETSTIIRGRWCCHKKEVPPIKSRNTQIKITFKSDDYFVAKPGFKIYY----- 119
Db 992 VYDTDSETSL---GRYCG-KSIPPSLTSSGNSILMVFVTDSD-LAYEGFLINYEISAAT 1046

QY 120 SLLEDFQPAASSET-----NWESVTSSISGVSYNSPSVTDPTTLIADALDKKIAEF 169
Db 1047 ACLQDYTDDLGTFTSPNFPNPNWECI-----YRI-TVRTGQLIA----- 1087

QY 170 DTVEDLLKYFNPSWQEDLENMYLDTPRYGRSY-----HDRK-- 207
Db 1088 -----VHFTNFSLEEAIGNYYTDFLEIRDGGYKESPLLGIIFYGNSLPTTIISHSNKLM 1140

QY 208 SKVDLRLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQRCGNGCGCTVNWRS 267
Db 1141 LKFKSDQI-DTRSGFSAYWDGSGTG-----CGGN----- 1168

QY 268 CTCNSGKTKVKYHVEVLQFEPGHI-----KRRGRAKTMALVDIQLDHHERC 312
Db 1169 LTTSSGTFISPNYPMPYHSSECYWMLKSSHGSFAFELEKDFHLEHHPNC 1218

RESULT 10
A39288
dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanog
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A39288
R;Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A;Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone
A;Reference number: A39288; MUID:92034970; PMID:1840509
A;Accession: A39288
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1057 <SHI>
A;Cross-references: UNIPROT:P25723; GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306
C;Genetics:
A;Gene: FlyBase:tld
A;Cross-references: FlyBase:FBgn0003719
C;Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repe
C;Keywords: duplication; hydrolase; metalloproteinase; zinc
F;136-329/Domain: astacin homology <AST>
F;352-464/Domain: C1r/C1s repeat homology <C1R1>
F;468-578/Domain: C1r/C1s repeat homology <C1R2>
F;585-620/Domain: EGF homology <EG1>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2004, 23:24:02 ; Search time 39 Seconds
(without alignments)
794.405 Million cell updates/sec

Title: US-10-086-623-6
Perfect score: 1742
Sequence: 1 LYRRDETIQVKGNGYVQSPR.....DIQLDHHERCDCICSSRPPR 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 1736 | 99.7 | 370 | 2 JC7591 | spinal cord-derive |
| 2 | 1567 | 90.0 | 370 | 2 JC7592 | spinal cord-derive |
| 3 | 1561 | 89.6 | 370 | 2 JC7998 | platelet-derived g |
| 4 | 193 | 11.1 | 823 | 1 A58788 | procollagen C-endo |
| 5 | 189.5 | 10.9 | 707 | 2 JC2218 | procollagen C-endo |
| 6 | 187.5 | 10.8 | 730 | 1 BMH1 | procollagen C-endo |
| 7 | 187.5 | 10.8 | 986 | 1 B58788 | procollagen C-endo |
| 8 | 187.5 | 10.8 | 991 | 2 I49540 | procollagen C-endo |
| 9 | 184.5 | 10.6 | 3623 | 2 T09456 | intrinsic factor-B |
| 10 | 174.5 | 10.0 | 1057 | 1 A39288 | dorsal-ventral pat |
| 11 | 172 | 9.9 | 3623 | 2 T08618 | intrinsic factor-B |
| 12 | 171.5 | 9.8 | 927 | 1 JQ0948 | A5 antigen precurs |
| 13 | 156.5 | 9.0 | 1524 | 2 T30337 | polypeptide - Afri |
| 14 | 151.5 | 8.7 | 1464 | 2 S58984 | development protei |
| 15 | 149 | 8.6 | 1070 | 2 T31069 | tolluid-BMP-1 like |
| 16 | 146.5 | 8.4 | 579 | 2 JC7629 | membrane-type friz |
| 17 | 146 | 8.4 | 686 | 1 A59271 | Ra-reactive factor |
| 18 | 141.5 | 8.1 | 767 | 2 T30018 | hypothetical prote |
| 19 | 138.5 | 8.0 | 1004 | 2 T30338 | oviductin (EC 3.4. |
| 20 | 138 | 7.9 | 2403 | 2 A59386 | sanko - human |
| 21 | 137.5 | 7.9 | 3871 | 2 T22812 | hypothetical prote |
| 22 | 137 | 7.9 | 276 | 2 A47290 | TSG-6 homolog PS4 |
| 23 | 136.5 | 7.8 | 449 | 2 A55362 | procollagen I C-pr |
| 24 | 135.5 | 7.8 | 699 | 1 I54763 | Ra-reactive factor |
| 25 | 133.5 | 7.7 | 597 | 2 S71352 | metalloproteinase |
| 26 | 130.5 | 7.5 | 402 | 2 JH0403 | procollagen I C-pr |
| 27 | 129 | 7.4 | 277 | 2 A41735 | hyaluronate-bindin |
| 28 | 127 | 7.3 | 705 | 1 C1HURB | complement subcomp |
| 29 | 125.5 | 7.2 | 533 | 2 JC7985 | brain-specific CUB |

| | | | | | |
|----|-------|-----|------|----------|--------------------|
| 30 | 123.5 | 7.1 | 275 | 2 JC6506 | tumor necrosis fac |
| 31 | 122.5 | 7.0 | 1290 | 2 A57190 | ebnerin precursor |
| 32 | 121 | 6.9 | 419 | 2 S69207 | vascular endotheli |
| 33 | 120.5 | 6.9 | 321 | 2 T33161 | hypothetical prote |
| 34 | 120.5 | 6.9 | 333 | 2 T21595 | hypothetical prote |
| 35 | 120 | 6.9 | 695 | 1 S05008 | complement subcomp |
| 36 | 118.5 | 6.8 | 1034 | 1 A53663 | enteropeptidase (E |
| 37 | 116.5 | 6.7 | 688 | 1 C1HUS | complement subcomp |
| 38 | 115.5 | 6.6 | 1594 | 2 T30549 | hensin - rabbit |
| 39 | 114.5 | 6.6 | 1019 | 1 A56318 | enteropeptidase (E |
| 40 | 114.5 | 6.6 | 1035 | 1 A43090 | enteropeptidase (E |
| 41 | 113 | 6.5 | 504 | 2 S56745 | mucin (clone pGM31 |
| 42 | 113 | 6.5 | 694 | 2 JC6554 | complement subcomp |
| 43 | 112 | 6.4 | 555 | 2 T21028 | hypothetical prote |
| 44 | 112 | 6.4 | 2083 | 2 T42721 | CRP-ductin-alpha p |
| 45 | 112 | 6.4 | 2197 | 2 B71600 | variant-specific s |

ALIGNMENTS

RESULT 1

JC7591
spinal cord-derived growth factor-B precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7591
R;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A;Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/1
A;Reference number: JC7591; MUID:21092670; PMID:11162582
A;Accession: JC7591
A;Molecule type: DNA
A;Residues: 1-370 <HAM>
A;Cross-references: UNIPROT:Q9BWV5; UNIPROT:Q9GZP0; DDBJ:AB033832
C;Genetics:
A;Gene: scdgf-B
F;1-17/Domain: secretory signal sequence #status predicted <SIG>
F;18-370/Product: spinal cord-derived growth factor-B #status predicted <SIG>
F;52-170/Region: CUB domain #status predicted
F;272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth
F;294-308/Region: conserved motif #status predicted

Query Match 99.7%; Score 1736; DB 2; Length 370;
Best Local Similarity 99.7%; Pred. No. 1.8e-127;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | LYRRDETIQVKGNGYVQSPRFPNPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI | 60 |
| Db | 49 | LYRRDETIQVKGNGYVQSPRFPNPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI | 108 |
| QY | 61 | CRYDFEVEDISETSTIIIRGRWCWGHEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYYS | 120 |
| Db | 109 | CRYDFEVEDISETSTIIIRGRWCWGHEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYYS | 168 |
| QY | 121 | LLEDFQPAASAETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN | 180 |
| Db | 169 | LLEDFQPAASAETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN | 228 |
| QY | 181 | PESWQEDLENMYLDTPRYGRSVHDKSKVDLDRNLDDAKRYSCITPRNYSVNIREELKLA | 240 |
| Db | 229 | PESWQEDLENMYLDTPRYGRSVHDKSKVDLDRNLDDAKRYSCITPRNYSVNIREELKLA | 288 |
| QY | 241 | NVVFPRCLLVQRCGNGCGGTVNRSCITCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA | 300 |
| Db | 289 | NVVFPRCLLVQRCGNGCGGTVNRSCITCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA | 348 |
| QY | 301 | LVDIQLDHHERCDCICSSRPPR | 322 |
| Db | 349 | LVDIQLDHHERCDCICSSRPPR | 370 |

RESULT 2

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2004, 23:15:59 ; Search time 191 Seconds
(without alignments)
970.003 Million cell updates/sec

Title: US-10-086-623-6
Perfect score: 1742
Sequence: 1 LYRRDETIQKNGYVQSPR.....DIQLDHERCDCICSSRPPR 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|------------|--------------------|
| 1 | 1742 | 100.0 | 364 | 2 | Q9BWV5 | Q9bwv5 homo sapien |
| 2 | 1742 | 100.0 | 364 | 2 | AAQ89474 | Aaq89474 homo sapi |
| 3 | 1742 | 100.0 | 370 | 2 | Q9GZP0 | Q9gzp0 homo sapien |
| 4 | 1567 | 90.0 | 370 | 2 | Q9EQT1 | Q9eqt1 rattus norv |
| 5 | 1561 | 89.6 | 370 | 2 | Q925I7 | Q925i7 mus musculu |
| 6 | 1493 | 85.7 | 300 | 2 | Q6V9H4 | Q6v9h4 oryctolagus |
| 7 | 1493 | 85.7 | 300 | 2 | AAQ24382 | Aaq24382 oryctolag |
| 8 | 965 | 55.4 | 261 | 2 | Q8K2L3 | Q8k2l3 mus musculu |
| 9 | 751.5 | 43.1 | 345 | 2 | Q9I946 | Q9i946 gallus gall |
| 10 | 750.5 | 43.1 | 345 | 2 | Q9QY71 | Q9qy71 m fallotein |
| 11 | 748.5 | 43.0 | 345 | 2 | Q8CI19 | Q8ci19 mus musculu |
| 12 | 742.5 | 42.6 | 345 | 2 | Q9EQX6 | Q9eqx6 rattus norv |
| 13 | 740.5 | 42.5 | 345 | 2 | Q9JHV8 | Q9jhv8 mus musculu |
| 14 | 739.5 | 42.5 | 345 | 2 | Q9UL22 | Q9ul22 homo sapien |
| 15 | 739.5 | 42.5 | 345 | 2 | Q9NRA1 | Q9nra1 homo sapien |
| 16 | 739.5 | 42.5 | 345 | 2 | AAQ88857 | Aaq88857 homo sapi |
| 17 | 632 | 36.3 | 258 | 2 | Q8K429 | Q8k429 rattus norv |
| 18 | 189.5 | 10.9 | 707 | 1 | BMP1_XENLA | P98070 xenopus lae |
| 19 | 189.5 | 10.9 | 977 | 2 | Q91925 | Q91925 xenopus lae |
| 20 | 188.5 | 10.8 | 735 | 2 | Q57381 | Q57381 xenopus lae |
| 21 | 187.5 | 10.8 | 241 | 2 | Q9Z135 | Q9zi35 rattus norv |
| 22 | 187.5 | 10.8 | 775 | 2 | Q6P550 | Q6p550 mus musculu |
| 23 | 187.5 | 10.8 | 775 | 2 | AAH63079 | Aah63079 mus muscu |
| 24 | 187.5 | 10.8 | 986 | 1 | BMP1_HUMAN | P13497 homo sapien |
| 25 | 187.5 | 10.8 | 991 | 1 | BMP1_MOUSE | P98063 mus musculu |
| 26 | 187.5 | 10.8 | 991 | 2 | Q6NZM2 | Q6nzm2 mus musculu |
| 27 | 187.5 | 10.8 | 991 | 2 | AAH66062 | Aah66062 mus muscu |
| 28 | 186.5 | 10.7 | 1015 | 2 | Q9Y6L7 | Q9y6l7 homo sapien |
| 29 | 186.5 | 10.7 | 1078 | 2 | Q9UQ00 | Q9uq00 homo sapien |
| 30 | 185 | 10.6 | 1007 | 2 | Q8JI28 | Q8ji28 xenopus lae |
| 31 | 184.5 | 10.6 | 3494 | 2 | Q7LC53 | Q7lc53 homo sapien |

| | | | | | | |
|----|-------|------|------|---|-----------|--------------------|
| 32 | 184.5 | 10.6 | 3623 | 2 | O60494 | O60494 homo sapien |
| 33 | 183.5 | 10.5 | 1012 | 2 | Q9WVM6 | Q9wvm6 mus musculu |
| 34 | 180.5 | 10.4 | 1022 | 1 | TLD_BRARE | O57460 brachydanio |
| 35 | 177 | 10.2 | 954 | 2 | Q7SÜQ6 | Q75ug6 achaearanae |
| 36 | 177 | 10.2 | 954 | 2 | BAD01492 | Bad01492 achaearan |
| 37 | 175.5 | 10.1 | 309 | 2 | Q6T495 | Q6t495 brachydanio |
| 38 | 175.5 | 10.1 | 309 | 2 | AAR99509 | Aar99509 brachydan |
| 39 | 175.5 | 10.1 | 3620 | 2 | Q9TU53 | Q9tu53 canis famil |
| 40 | 175 | 10.0 | 871 | 2 | Q6T869 | Q6t869 brachydanio |
| 41 | 175 | 10.0 | 871 | 2 | AAR99506 | Aar99506 brachydan |
| 42 | 175 | 10.0 | 959 | 2 | Q6RT22 | Q6rt22 brachydanio |
| 43 | 175 | 10.0 | 959 | 2 | Q6T870 | Q6t870 brachydanio |
| 44 | 175 | 10.0 | 959 | 2 | AAR89616 | Aar89616 brachydan |
| 45 | 175 | 10.0 | 959 | 2 | AAR99505 | Aar99505 brachydan |

ALIGNMENTS

RESULT 1
Q9BWV5 ID Q9BWV5 PRELIMINARY; PRT; 364 AA.
AC Q9BWV5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Iris-expressed growth factor short form (Platelet derived growth factor D, isoform 2) (SCDGF-B).
GN Name=IEGF; Synonyms=PDGFD; ORFNames=UNQ1899;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W., Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal pigment epithelium";
RT Mol. Vision 8:185-195(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg-R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]

RN SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY027518; AAK20082.1; -.
DR EMBL; BC030645; AAH30645.1; -.
DR EMBL; AY359116; AAQ89474.1; -.
DR PIR; JC7591; JC7591.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 364 AA; 42166 MW; 245C53E8DDEA9EAC_CRC64;

Query Match 100.0%; Score 1742; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 3e-129;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRDETIQVKGNGYVQSPRFPNSYPNRLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db 43 LYRDETIQVKGNGYVQSPRFPNSYPNRLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 102
QY 61 CRYDFVEVEDISETSTIIRGRWCGHKEVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 120
Db 103 CRYDFVEVEDISETSTIIRGRWCGHKEVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDQFQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 180
Db 163 LLEDQFQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCTPRNYSVNIREELKLA 240
Db 223 PESWQEDLENMYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCTPRNYSVNIREELKLA 282
QY 241 NVVFFPRCLLVQRCGCGCGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 283 NVVFFPRCLLVQRCGCGCGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 342
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db 343 LVDIQLDHHERCDCICSSRPPR 364

RESULT 2
AAQ89474
ID AAQ89474 PRELIMINARY; PRT; 364 AA.
AC AAQ89474;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE SCDGF-B.
GN UNQ1899.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY359116; AAQ89474.1; -.
SQ SEQUENCE 364 AA; 42166 MW; 245C53E8DDEA9EAC_CRC64;

Query Match 100.0%; Score 1742; DB 2; Length 364;
Best Local Similarity 100.0%; pred. No. 3e-129;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRDETIQVKGNGYVQSPRFPNSYPNRLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db 43 LYRDETIQVKGNGYVQSPRFPNSYPNRLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 102
QY 61 CRYDFVEVEDISETSTIIRGRWCGHKEVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 120
Db 103 CRYDFVEVEDISETSTIIRGRWCGHKEVPPIKSRNQIKITFKSDDYFVAKPGFKIYYS 162
QY 121 LLEDQFQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 180
Db 163 LLEDQFQAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 222
QY 181 PESWQEDLENMYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCTPRNYSVNIREELKLA 240
Db 223 PESWQEDLENMYLDTPRYGRSYHDKRSKVDLDRNLDDAKRYSCTPRNYSVNIREELKLA 282
QY 241 NVVFFPRCLLVQRCGCGCGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 283 NVVFFPRCLLVQRCGCGCGTNNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 342
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db 343 LVDIQLDHHERCDCICSSRPPR 364

RESULT 3
Q9GZP0
ID Q9GZP0 PRELIMINARY; PRT; 370 AA.
AC Q9GZP0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Spinal cord-derived growth factor-B (MSTP036) (Platelet-derived growth
DE factor D) (Iris-expressed growth factor long form).
GN Name=hSCDGF-B; Synonyms=IEGF, PDGFD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RN SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RT SCDGF/PDGF-C/fallotain.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
RN [2]
Rn SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,

RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.,
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231380; PubMed=11331882;
RA LaRochele W.J., Jeffers M., McDonald W.F., Chillakuru R.A., Vernet C.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M.,
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
RA Shimkets R.A., Rothberg J.M., Lichenstein H.S.,
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11331881;
RA Bergsten E., Untela M., Li X., Pietras K., Ostman A., Heldin C.H.,
RA Alitalo K., Eriksson U.,
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
RT receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA Bouffard G., Smith D., Peterson K.,
RT "Expressed sequence tag analysis of adult human iris for the NEIBank
RT Project: steroid-response factors and similarities with retinal
RT pigment epithelium.";
RL Mol. Vision 8:185-195(2002).
DR EMBL; AB033832; BAB18903.1; -.
DR EMBL; AF113216; AAG39287.1; -.
DR EMBL; AF335584; AAK38840.1; -.
DR EMBL; AF336376; AAK56136.1; -.
DR EMBL; AY027517; AAK20081.1; -.
DR PIR; JC7591; JC7591.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674_CRC64;

Query Match 100.0%; Score 1742; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.1e-129;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRRDETIQVKGNGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db 49 LYRRDETIQVKGNGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 108

QY 61 CRYDFEVEDISETSTIIRGRWCWGHEVPPIKSRITNQIKITFKSDDDYFVAKPGFKIYYS 120
Db 109 CRYDFEVEDISETSTIIRGRWCWGHEVPPIKSRITNQIKITFKSDDDYFVAKPGFKIYYS 168

QY 121 LLEDQPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN 180
Db 169 LLEDQPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN 228

QY 181 PESWQEDLENMYLDTPRYGRSYPHDKSKVDLRLNDDAKRYSCPTPRNYSVNIREELKLA 240
Db 229 PESWQEDLENMYLDTPRYGRSYPHDKSKVDLRLNDDAKRYSCPTPRNYSVNIREELKLA 288

QY 241 NVVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 289 NAVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348

Db 289 NVVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348
QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db 349 LVDIQLDHHERCDCICSSRPPR 370

RESULT 4
Q9EQT1
ID Q9EQT1 PRELIMINARY; PRT; 370 AA.
AC Q9EQT1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN Name=rSCDGF-B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.,
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RT SCDGF/PDGF-C/fallotein.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
DR EMBL; AB052170; BAB18920.1; -.
DR PIR; JC7592; JC7592.
DR HSSP; Q9UCV4; INZI.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73_CRC64;

Query Match 90.0%; Score 1567; DB 2; Length 370;
Best Local Similarity 87.0%; Pred. No. 2.1e-115;
Matches 280; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

QY 1 LYRRDETIQVKGNGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 60
Db 49 LYRRDENIRVTGTGHVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDI 108

QY 61 CRYDFEVEDISETSTIIRGRWCWGHEVPPIKSRITNQIKITFKSDDDYFVAKPGFKIYYS 120
Db 109 CRYDFEVEDISETSTIIRGRWCWGHEVPPIKSRITNQIKITFKSDDDYFVAKPGFKIYYS 168

QY 121 LLEDQPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFN 180
Db 169 FVEDFQPEAAASEINWESVTSSISGVSYNSPSVMDSTLTADALDKKIAEFTVEDLLKYFN 228

QY 181 PESWQEDLENMYLDTPRYGRSYPHDKSKVDLRLNDDAKRYSCPTPRNYSVNIREELKLA 240
Db 229 PASWQDDLENMYLDTPRYGRSYPHDKSKVDLRLNDDAKRYSCPTPRNYSVNIREELKLT 288

QY 241 NVVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
Db 289 NAVFFPRCLLVQRCGNGCGGTNNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 348

QY 301 LVDIQLDHHERCDCICSSRPPR 322
Db 349 LVDIQLDHHERCDCICSSRPPR 370

RESULT 5
Q925I7

| | | | |
|---|--|--|--------------|
| QY | 121 | LLEDFOPAASSETNWESVTSSISGVSYNSPSPVTDPTLIADALDKKIAEFTVEDLLKYFN | 180 |
| Db | 169 | FVEDSQPEAASETNWESVTSSFSGVSYHSPSITDPTLTADALDKTVAEFTVEDLLKHFN | 228 |
| QY | 181 | PESWQEDLENMYLDTPRYGRGRSYHDKRSK | 209 |
| Db | 229 | PVSWQDDLENLYLDTPHYRGRGRSYHDKRSK | 257 |
| RESULT 9 | | | |
| ID | Q9I946 | PRELIMINARY; | PRT; 345 AA. |
| AC | Q9I946; | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Created) | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | | |
| DE | Spinal cord-derived growth factor. | | |
| GN | Name=SCDGF; | | |
| OS | Gallus gallus (Chicken). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; | | |
| OC | Gallus. | | |
| OX | NCBI_TaxID=9031; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=white leghorn; TISSUE=Spinal cord; | | |
| RX | MEDLINE=20317014; PubMed=10858496; | | |
| RA | Hamada T., Ui-Tei K., Miyata Y.; | | |
| RT | "A novel gene derived from developing spinal cords, SCDGF, is a unique | | |
| RT | member of the PDGF/VEGF family."; | | |
| RL | FEBS Lett. 475:97-102(2000). | | |
| CC | -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family. | | |
| DR | EMBL; AB033829; BAB03265.1; -. | | |
| DR | HSSP; Q9UCV4; INZI. | | |
| DR | GO; GO:0016020; C:membrane; IEA. | | |
| DR | GO; GO:0008083; F:growth factor activity; IEA. | | |
| DR | GO; GO:0008151; P:cell growth and/or maintenance; IEA. | | |
| DR | InterPro; IPR000859; CUB. | | |
| DR | InterPro; IPR000072; PD_growth_factor. | | |
| DR | Pfam; PF00431; CUB; 1. | | |
| DR | Pfam; PF00341; PDGF; 1. | | |
| DR | ProDom; PD001629; PD_growth_factor; 1. | | |
| DR | SMART; SM00042; CUB; 1. | | |
| DR | SMART; SM00141; PDGF; 1. | | |
| DR | PROSITE; PS01180; CUB; 1. | | |
| DR | PROSITE; PS0278; PDGF 2; 1. | | |
| KW | Growth factor; Mitogen. | | |
| SQ | SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64; | | |
| Query Match 43.1%; Score 751.5; DB.2; Length 345; | | | |
| Best Local Similarity 47.0%; Pred. No. 5e-51; | | | |
| Matches 150; Conservative 53; Mismatches 87; Indels 29; Gaps 8; | | | |
| QY | 3 | RRDETIOVKNGYVQSPREFNSYPNLLLTWRLHS-QENTRIQLVFDNQFGLLEEAENDIC | 61 |
| Db | 45 | QHEKIITVTSNGSIHSPKFPHTYPNTVLVWRLVAVDENVMWQLTFDERFGLEDPEDDIC | 104 |
| QY | 62 | RYDFVEVEDISETSTIIRGRWCCHKVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYVSL | 121 |
| Db | 105 | KYDFVEVEEPSDGTVL--GRWCGSSVPSRQISKGNQIRIRFVSDEYFSPQPGFCIHVTL | 162 |
| QY | 122 | LEDFOPAASSETNWESVTSSISGVSYNSPSPVTDPT-LIADALDKKIAEFTVEDLLKYFN | 180 |
| Db | 163 | LVPHTTEAP-----SPSSLPPSALPLDLVNNAVAGFSTVEELIRYLE | 204 |
| QY | 181 | PESWQEDLENMYLDTPRYGRGRSY-HDKRSK-VLDRLNDDAKRYSCTPRNYSVNIREELK | 238 |
| Db | 205 | PDRWQLDLEDLYRPTWQLLGKAYIHGRKSRVVDLNLKKEVRVLYSCTPRNFSVSLREELK | 264 |
| QY | 239 | LANVVFPRCLLVQRCGGNCGGCTGVNWSCTNSGKTVKKYHEVLQFEPGHKRRG-RAK | 297 |
| Db | 265 | RTDTIFWPLCLLVKRCGGNCACCHQNCNECQCIPTKVTKKYHEVLQLKP----RSGVRGL | 320 |

| | | | |
|-----------|--|---------------------|--------------|
| QY | 298 | TMALVDIQLDHHERCDCIC | 316 |
| Db | 321 | HKSLTDVPLEHHEECDCVC | 339 |
| RESULT 10 | | | |
| ID | Q9QY71 | PRELIMINARY; | PRT; 345 AA. |
| AC | Q9QY71; | | |
| DT | 01-MAY-2000 (TrEMBLrel. 13, Created) | | |
| DT | 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) | | |
| DT | 01-OCT-2004 (TrEMBLrel. 28, Last annotation update) | | |
| DE | Fallopein (Platelet-derived growth factor C) (Mus musculus adult male | | |
| DE | cecum cDNA, RIKEN full-length enriched library, clone:9130403O08 | | |
| DE | product:platelet-derived growth factor, C polypeptide, full insert | | |
| DE | sequence) (Mus musculus 7 days neonate cerebellum cDNA, RIKEN full- | | |
| DE | length enriched library, clone:A730022G11 product:platelet-derived | | |
| DE | growth factor, C polypeptide, full insert sequence) (Mus musculus 15 | | |
| DE | days embryo head cDNA, RIKEN full-length enriched library, C | | |
| DE | clone:D930001M08 product:platelet-derived growth factor, C | | |
| DE | polypeptide, full insert sequence). | | |
| GN | Name=Pdgfc; | | |
| OS | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| OX | NCBI_TaxID=10090; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=Ovary; | | |
| RA | Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.; | | |
| RL | Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases. | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=C57BL/6J; | | |
| RA | Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K., | | |
| RA | Gilbertson D., West J., O'Hara P.J.; | | |
| RL | Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases. | | |
| RN | [3] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head; | | |
| RX | MEDLINE=99279253; PubMed=10349636; | | |
| RA | Carninci P., Hayashizaki Y.; | | |
| RT | "High-efficiency full-length cDNA cloning."; | | |
| RL | Meth. Enzymol. 303:19-44(1999). | | |
| RN | [4] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head; | | |
| RX | MEDLINE=21085660; PubMed=11217851; | | |
| RA | RIKEN FANTOM Consortium; | | |
| RT | "Functional annotation of a full-length mouse cDNA collection."; | | |
| RL | Nature 409:685-690(2001). | | |
| RN | [5] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head; | | |
| RA | The FANTOM Consortium, | | |
| RA | the RIKEN Genome Exploration Research Group Phase I & II Team; | | |
| RT | "Analysis of the mouse transcriptome based on functional annotation of | | |
| RT | 60,770 full-length cDNAs."; | | |
| RL | Nature 420:563-573 (2002). | | |
| RN | [6] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head; | | |
| RX | MEDLINE=20499374; PubMed=11042159; | | |
| RA | Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., | | |
| RA | Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; | | |
| RT | "Normalization and subtraction of cap-trapper-selected cDNAs to | | |
| RT | prepare full-length cDNA libraries for rapid discovery of new genes."; | | |
| RL | Genome Res. 10:1617-1630(2000). | | |
| RN | [7] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head; | | |
| RX | MEDLINE=20530913; PubMed=11076861; | | |
| RA | Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., | | |

Db 45 RHERVVTISNGSIHSPKFPTYPRNMVLVWRLVAVDENVRITQLTDFDERFGLDEPDDL 104
QY 62 RYDFVEVEDISETSTIIRGRCWGHEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYVSL 121
Db 105 KYDFVEVEEPSDGSVL--GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSI 162
QY 122 LEDFQPAASETWNESVTSSISGVSNPSVTDPTLIA-DALDKKIAEFTVEDLLKYFN 180
Db 163 I---MPQVTETT-----SPSVLPSSLSLDLNNAVTAFSTLEELIRYLE 204
QY 181 PESWOEDLENMYLDTPRYGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELK 238
Db 205 PDRWQVDLDSLYKPTWQLLGKAFLYGKSKAVNLLKKEEVKLYSCTPRNFSVSIREELK 264
QY 239 LANVVFPRCLLVQRCGNGCGGTVMNRSCTNSGKTVMKKYHEVLQFEPGHIKRRGRAKT 298
Db 265 RTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP---KTGVKGLH 321
QY 299 MALVDIQLDHHERCDCIC 316
Db 322 KSLTDVALEHHEECDCVC 339

RESULT 12
Q9EQX6
ID Q9EQX6 PRELIMINARY; PRT; 345 AA.
AC Q9EQX6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=rScdGF;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=21092670; PubMed=11162582;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/fallotein.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AB033830; BAB19969.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;

Query Match 42.6%; Score 742.5; DB 2; Length 345;
Best Local Similarity. 45.6%; Pred. No. 2.6e-50;
Matches 145; Conservative 59; Mismatches 87; Indels 27; Gaps 9;

QY 3 RRDETIQKNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLAEAENDIC 61
Db 45 RHERVVTISNGSIHSPKFPTYPRNTVLVWRLVAVDENVRITQLTDFDERFGLDEPDDL 104
QY 62 RYDFVEVEDISETSTIIRGRCWGHEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYVSL 121
Db 105 KYDFVEVEEPSDGSVL--GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSI 162

QY 122 LEDFQPAASETWNESVTSSISGVSNPSVTDPTLIA-DALDKKIAEFTVEDLLKYFN 180
Db 163 I---MPQVTETT-----SPSVLPSSLSLDLNNAVTAFSTVEELIRFLE 204
QY 181 PESWOEDLENMYLDTPRYGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELK 238
Db 205 PDRWQVDLDSLYKPTWQLLGKAFLYGKSKAVNLLKKEEVKLYSCTPRNFSVSIREELK 264
QY 239 LANVVFPRCLLVQRCGNGCGGTVMNRSCTNSGKTVMKKYHEVLQFEPGHIKRRGRAKT 298
Db 265 RTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP-KIGVKGLHK- 322
QY 299 MALVDIQLDHHERCDCIC 316
Db 323 -SLTDVALEHHEECDCVC 339

RESULT 13
Q9JHV8
ID Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
GN Name=PDGfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RX MEDLINE=20417814; PubMed=10960785;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during organogenesis.";
RL Mech. Dev. 96:209-213(2000).
DR EMBL; AF286725; AAF91483.1; -.
DR MGD; MGI:1859631; PdGfc.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005161; F:platelet-derived growth factor receptor bin. . .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;

Query Match 42.5%; Score 740.5; DB 2; Length 345;
Best Local Similarity 45.3%; Pred. No. 3.7e-50;
Matches 144; Conservative 58; Mismatches 89; Indels 27; Gaps 8;

QY 3 RRDETIQKNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLAEAENDIC 61
Db 45 RHERVVTISNGSIHSPKFPTYPRNMVLVWRLVAVDENVRITQLTDFDERFGLDEPDDL 104
QY 62 RYDFVEVEDISETSTIIRGRCWGHEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYVSL 121
Db 105 KYDFVEVEEPSDGSVL--GRWCGSETVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSI 162
QY 122 LEDFQPAASETWNESVTSSISGVSNPSVTDPTLIA-DALDKKIAEFTVEDLLKYFN 180
Db 163 I---MPQVTETT-----SPSVLPSSLSLDLNNAVTAFSTLEELIRYLE 204
QY 181 PESWOEDLENMYLDTPRYGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELK 238
Db 205 PDRWQVDLDSLYKPTWQLLGKAFLYVKKSVNLLKKEEVKLYSCTPRNFSVSIREELK 264

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:52:57 ; Search time 186 Seconds
(without alignments)
7390.676 Million cell updates/sec

Title: US-10-086-623-5
Perfect score: 1934
Sequence: 1 ttgtaccgaagagatgagac.....atcgacgtaactggaaccg 1934

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------|
| 1 | 1934 | 100.0 | 1934 | 4 | US-09-438-046-5 |
| 2 | 1934 | 100.0 | 2253 | 4 | US-09-438-046-7 |
| 3 | 1491.8 | 77.1 | 1882 | 4 | US-09-457-066-36 |
| 4 | 1491.8 | 77.1 | 1882 | 4 | US-09-540-224-1 |
| 5 | 1491.8 | 77.1 | 1882 | 4 | US-09-564-595D-1 |
| 6 | 1491.8 | 77.1 | 1882 | 4 | US-09-706-968-36 |
| 7 | 1491.8 | 77.1 | 1882 | 4 | US-09-808-972-1 |
| 8 | 1003.4 | 51.9 | 1162 | 4 | US-10-140-002-185 |
| 9 | 795.4 | 41.1 | 1472 | 4 | US-09-540-224-3 |
| 10 | 795.4 | 41.1 | 1472 | 4 | US-09-564-595D-52 |
| 11 | 795.4 | 41.1 | 1472 | 4 | US-09-808-972-3 |
| 12 | 697.6 | 36.1 | 1110 | 4 | US-09-564-595D-6 |
| 13 | 662 | 34.2 | 690 | 4 | US-09-438-046-3 |
| 14 | 355.2 | 18.4 | 360 | 4 | US-09-438-046-1 |
| 15 | 213.8 | 11.1 | 256 | 3 | US-09-222-575-13 |
| 16 | 213.8 | 11.1 | 256 | 4 | US-09-389-681-13 |
| 17 | 213.8 | 11.1 | 256 | 4 | US-09-620-405B-13 |
| 18 | 213.8 | 11.1 | 256 | 4 | US-09-339-338-13 |
| 19 | 213.8 | 11.1 | 256 | 4 | US-09-433-826B-13 |
| 20 | 213.8 | 11.1 | 256 | 4 | US-09-604-287A-13 |
| 21 | 213.8 | 11.1 | 256 | 4 | US-09-285-480-13 |
| 22 | 213.8 | 11.1 | 256 | 4 | US-09-834-759-13 |
| 23 | 213.8 | 11.1 | 256 | 4 | US-09-590-751A-13 |
| 24 | 181.8 | 9.4 | 1035 | 4 | US-09-457-066-6 |
| 25 | 181.8 | 9.4 | 1035 | 4 | US-09-706-968-6 |
| 26 | 123.2 | 6.4 | 3571 | 4 | US-09-457-066-42 |
| 27 | 123.2 | 6.4 | 3571 | 4 | US-09-564-595D-34 |

| | | | | | | |
|----|-------|-----|------|---|--------------------|-------------------|
| 28 | 123.2 | 6.4 | 3571 | 4 | US-09-706-968-42 | Sequence 42, Appl |
| 29 | 123.2 | 6.4 | 3571 | 4 | US-09-823-033-3 | Sequence 3, Appl |
| 30 | 104 | 5.4 | 1760 | 4 | US-09-457-066-1 | Sequence 1, Appl |
| 31 | 104 | 5.4 | 1760 | 4 | US-09-564-595D-32 | Sequence 32, Appl |
| 32 | 104 | 5.4 | 1760 | 4 | US-09-706-968-1 | Sequence 1, Appl |
| 33 | 104 | 5.4 | 1760 | 4 | US-09-823-033-1 | Sequence 1, Appl |
| 34 | 104 | 5.4 | 2825 | 3 | US-09-040-220D-1 | Sequence 1, Appl |
| 35 | 104 | 5.4 | 2825 | 4 | US-09-265-686-1 | Sequence 1, Appl |
| 36 | 104 | 5.4 | 2825 | 4 | US-09-723-749-1 | Sequence 1, Appl |
| 37 | 104 | 5.4 | 2849 | 4 | US-10-140-002-285 | Sequence 285, App |
| 38 | 102.2 | 5.3 | 1095 | 4 | US-09-457-066-50 | Sequence 50, Appl |
| 39 | 102.2 | 5.3 | 1095 | 4 | US-09-706-968-50 | Sequence 50, Appl |
| 40 | 100.6 | 5.2 | 1035 | 4 | US-09-468-647-3 | Sequence 3, Appl |
| 41 | 75.4 | 3.9 | 504 | 4 | US-09-468-647-28 | Sequence 28, Appl |
| 42 | 63 | 3.3 | 1141 | 4 | US-09-806-708B-22 | Sequence 22, Appl |
| 43 | 57.6 | 3.0 | 452 | 4 | US-09-621-976-1352 | Sequence 1352, Ap |
| 44 | 57 | 2.9 | 1141 | 4 | US-09-806-708B-22 | Sequence 22, Appl |
| 45 | 54.8 | 2.8 | 6306 | 4 | US-10-204-708-50 | Sequence 50, Appl |

ALIGNMENTS

RESULT 1
US-09-438-046-5
; Sequence 5, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver: 2.0
; SEQ ID NO 5
; LENGTH: 1934
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(966)
US-09-438-046-5

Query Match 100.0%; Score 1934; DB 4; Length 1934;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1934; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
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| QY | 1 | TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTACGTGCAGAGTCCTAGA | 60 |
| Db | 1 | TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTACGTGCAGAGTCCTAGA | 60 |
| QY | 61 | TTCCCGAACAGCTACCCAGGAACCTGCTCTTGACATGGCGGCTTCACTCTCAGGAGAAT | 120 |
| Db | 61 | TTCCCGAACAGCTACCCAGGAACCTGCTCTTGACATGGCGGCTTCACTCTCAGGAGAAT | 120 |

QY 121 ACACGGATACAGCTAGTGTGTTTGACAATCAGTTTGGATTAGAGGAACAGAAAATGATATC 180
Db |||||
QY 121 ACACGGATACAGCTAGTGTGTTTGACAATCAGTTTGGATTAGAGGAACAGAAAATGATATC 180
Db |||||
QY 181 TGTAGGTATGATTTTGTGGAAAGTTGAAAGATATATCCGAAAACCGATACCATTATTAGAGGA 240
Db |||||
QY 181 TGTAGGTATGATTTTGTGGAAAGTTGAAAGATATATCCGAAAACCGATACCATTATTAGAGGA 240
Db |||||
QY 241 CGATGGTGTGGACACAAAGAAAGTTTCCCTCAAGGATAAAATCAAGAACGAAACCAAAATTAAA 300
Db |||||
QY 241 CGATGGTGTGGACACAAAGAAAGTTTCCCTCAAGGATAAAATCAAGAACGAAACCAAAATTAAA 300
Db |||||
QY 301 ATCACATTCAGTCCGATGACTACTTTGTGGCTTAAACCTGGATTCAAGATTATTATTCT 360
Db |||||
QY 301 ATCACATTCAGTCCGATGACTACTTTGTGGCTTAAACCTGGATTCAAGATTATTATTCT 360
Db |||||
QY 361 TTGCTGGAAGATTTCCAAACCCGACGAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 420
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QY 361 TTGCTGGAAGATTTCCAAACCCGACGAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 420
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QY 421 TCTATTTACGGGTATCCTTAACTCTCCATCAGTAACGGATCCCACCTCTGATGCGGAT 480
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QY 421 TCTATTTACGGGTATCCTTAACTCTCCATCAGTAACGGATCCCACCTCTGATGCGGAT 480
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QY 481 GCTCTGGACAAAAAATTGCAGAAATTGATACAGTGGAGATCTGTCTCAAGTACTTCAAT 540
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QY 601 AGGTATACCATGACCCGAAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
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QY 661 CGTTACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGCTGAAGTTGGCC 720
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QY 661 CGTTACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGCTGAAGTTGGCC 720
Db |||||
QY 721 AATGTGGTCTTCTTTCCAGTTCCTCGTGCAGCGCTGTGAGGAAATTTGTGGCTGT 780
Db |||||
QY 721 AATGTGGTCTTCTTTCCAGTTCCTCGTGCAGCGCTGTGAGGAAATTTGTGGCTGT 780
Db |||||
QY 781 GGAACCTGTCAACTGGAGGTCTTGACATGCAATTCAGGGAAACCGTGAAAGTATCAT 840
Db |||||
QY 781 GGAACCTGTCAACTGGAGGTCTTGACATGCAATTCAGGGAAACCGTGAAAGTATCAT 840
Db |||||
QY 841 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGTAAAGACCATGGCT 900
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QY 841 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGTAAAGACCATGGCT 900
Db |||||
QY 901 CTAGTTGACATCCAGTTGGATCACCATTGAACGATGCGATTGTATCTGCAGCTCAAGACCA 960
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QY 901 CTAGTTGACATCCAGTTGGATCACCATTGAACGATGCGATTGTATCTGCAGCTCAAGACCA 960
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QY 961 CCTCGATAAGAGAATGTGCACATCCTTACATTAAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020
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QY 961 CCTCGATAAGAGAATGTGCACATCCTTACATTAAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020
Db |||||
QY 1021 GGGTGAGATAAGAGACCCCTTTCTACCAGCAACCAACTTACTACTAGCTGCAATGCA 1080
Db |||||
QY 1021 GGGTGAGATAAGAGACCCCTTTCTACCAGCAACCAACTTACTACTAGCTGCAATGCA 1080
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QY 1081 ATGAACACAAGTGGTTGCTGAGTCTCAGCCCTTGTGTTAATGCCATGCAAGTAGAAA 1140
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QY 1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTCATTAAATAGTGTGAG 1200
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QY 1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTCATTAAATAGTGTGAG 1200
Db |||||

QY 1201 GTTATATATGCACAAACACACACAGAAATATATTCTATGTGTATATAGATCAAT 1260
Db |||||
QY 1201 GTTATATATGCACAAACACACACAGAAATATATTCTATGTGTATATAGATCAAT 1260
Db |||||
QY 1261 GTTTTGTGTAATATAAACCCAGGTACACAGAGCTTACATATGTTGAGTTAGACTCT 1320
Db |||||
QY 1261 GTTTTGTGTAATATAAACCCAGGTACACAGAGCTTACATATGTTGAGTTAGACTCT 1320
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QY 1321 TAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAATTT 1380
Db |||||
QY 1321 TAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAAATTT 1380
Db |||||
QY 1381 AGGAGATAAAATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGTCTCTTTA 1440
Db |||||
QY 1381 AGGAGATAAAATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGTCTCTTTA 1440
Db |||||
QY 1441 AAGAAAGCATCTTGATATATAAAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG 1500
Db |||||
QY 1441 AAGAAAGCATCTTGATATATAAAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG 1500
Db |||||
QY 1501 TTGATTTTAAAAAAGGAAAAAGGTTTCCAGAGAAAAAGCCAAATACCTAAGCAATTTTTC 1560
Db |||||
QY 1501 TTGATTTTAAAAAAGGAAAAAGGTTTCCAGAGAAAAAGCCAAATACCTAAGCAATTTTTC 1560
Db |||||
QY 1561 CATGAGAACCATGTCATACCTTATGCTGAGCTGTAACTGTCTCCAAAAACCATGC 1620
Db |||||
QY 1561 CATGAGAACCATGTCATACCTTATGCTGAGCTGTAACTGTCTCCAAAAACCATGC 1620
Db |||||
QY 1621 CATAATATAAAGTCTTTAGAAATTAATCATTTGCTGTTTATGCAATTTTGTCTGAGG 1680
Db |||||
QY 1621 CATAATATAAAGTCTTTAGAAATTAATCATTTGCTGTTTATGCAATTTTGTCTGAGG 1680
Db |||||
QY 1681 CATCCTTATTCATTTAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTATTATAGTC 1740
Db |||||
QY 1681 CATCCTTATTCATTTAACACCTATCTCAAAAACTTACTTAGAAGGTTTTTATTATAGTC 1740
Db |||||
QY 1741 CTACAAAAGACAATGTATAAGCTGTAACTGTAACTGTAACTGTAACTGTAACTGTAACTGT 1800
Db |||||
QY 1741 CTACAAAAGACAATGTATAAGCTGTAACTGTAACTGTAACTGTAACTGTAACTGTAACTGT 1800
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QY 1801 CTCCACAAAAGCAAAATCCTTTCAAGATGGCATGGGCAATCTGTATGAACCTTTCCAGAT 1860
Db |||||
QY 1801 CTCCACAAAAGCAAAATCCTTTCAAGATGGCATGGGCAATCTGTATGAACCTTTCCAGAT 1860
Db |||||
QY 1861 GGTGTTCAAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAACATCGAC 1920
Db |||||
QY 1861 GGTGTTCAAGTGAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAACATCGAC 1920
Db |||||
QY 1921 GTAACCTGGAAACCG 1934
Db |||||
QY 1921 GTAACCTGGAAACCG 1934
Db |||||

RESULT 2
US-09-438-046-7
; Sequence 7, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10

; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2253
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (176)..(1288)
US-09-438-046-7

Query Match 100.0%; Score 1934; DB 4; Length 2253;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1934; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAAACGGCTACGTGCAGAGTCCTAGA 60
Db 320 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAAACGGCTACGTGCAGAGTCCTAGA 379

Qy 61 TTCCCGAACAGCTACCCCGAGGAACCTGCTCCTGACATGGCGGCTTCACCTCTCAGGAGAA 120
Db 380 TTCCCGAACAGCTACCCCGAGGAACCTGCTCCTGACATGGCGGCTTCACCTCTCAGGAGAA 439

Qy 121 ACACGGATACAGCTAGTGTGTTTGACAAATCAGTTGGATTAGAGGAAGCAGAAAATGATATC 180
Db 440 ACACGGATACAGCTAGTGTGTTTGACAAATCAGTTGGATTAGAGGAAGCAGAAAATGATATC 499

Qy 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTATTAGAGGA 240
Db 500 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTATTAGAGGA 559

Qy 241 CGATGGTGTGGACACAAGGAAGTTCCCTCCAGGATAAAAATCAAGAACGACCAAAATTAAA 300
Db 560 CGATGGTGTGGACACAAGGAAGTTCCCTCCAGGATAAAAATCAAGAACGACCAAAATTAAA 619

Qy 301 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 360
Db 620 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 679

Qy 361 TTGCTGGAAGATTTCCAAACCCGACGACTTCAGAGACCAACTGGGAATCTGTCACAAGC 420
Db 680 TTGCTGGAAGATTTCCAAACCCGACGACTTCAGAGACCAACTGGGAATCTGTCACAAGC 739

Qy 421 TCTATTTCAGGGGTATCCTATAAATCTCCATCAGTAACGGATCCCACCTCGATTGCGGAT 480
Db 740 TCTATTTCAGGGGTATCCTATAAATCTCCATCAGTAACGGATCCCACCTCGATTGCGGAT 799

Qy 481 GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 540
Db 800 GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGAAGATCTGCTCAAGTACTTCAAT 859

Qy 541 CCAGAGTCATGGCAAGAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 860 CCAGAGTCATGGCAAGAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 919

Qy 601 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db 920 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 979

Qy 661 CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAAAGAGCTGAAGTTGGCC 720
Db 980 CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAAAGAGCTGAAGTTGGCC 1039

Qy 721 AATGTGGTCTTCTTTCCAGCTTGCCCTCCTCGTGCAGCGCTGTGGAGGAAATTTGGGCTGT 780

Db 1040 AATGTGGTCTTCTTTCCAGCTTGCCCTCCTCGTGCAGCGCTGTGAGGAAAAATTGTGGCTGT 1099
Qy 781 GGAACCTGCAAACTGGAGGTCCTGCACATGCAATTCAGGGAAAAACCGTGAAGAAAGTATCAT 840
Db 1100 GGAACCTGCAAACTGGAGGTCCTGCACATGCAATTCAGGGAAAAACCGTGAAGAAAGTATCAT 1159
Qy 841 GAGGTATTACAGTTTGAGCCCTGSCCAGATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900
Db 1160 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 1219
Qy 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATCGGATTGTATCTGCAGCTCAAGACCA 960
Db 1220 CTAGTTGACATCCAGTTGGATCACCATGAACGATCGGATTGTATCTGCAGCTCAAGACCA 1279
Qy 961 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTTAGTTTAAGGA 1020
Db 1280 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTTAGTTTAAGGA 1339
Qy 1021 GGGTGAGATAAGAGACCCCTTTTCCCTACCAGCAACCAACCTTACTACTAGCCTGCAANTGCA 1080
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Qy 1081 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1140
Db 1400 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1459
Qy 1141 GGTATATCATCAACTTCTATACCTTAAGAAATATAGGATTGCAATTTAATAATAGTGTGAG 1200
Db 1460 GGTATATCATCAACTTCTATACCTTAAGAAATATAGGATTGCAATTTAATAATAGTGTGAG 1519
Qy 1201 GTTATATATGCAAAAACACACACAGAAATATATTATTCATGTCTATGTGTATATAGATCAAA 1260
Db 1520 GTTATATATGCAAAAACACACACAGAAATATATTATTCATGTCTATGTGTATATAGATCAAA 1579
Qy 1261 GTTTTTTTTGGTATATATAACCAGGTACACAGAGCTTACATATGTTTGGATTAGACTCT 1320
Db 1580 GTTTTTTTTGGTATATATAACCAGGTACACAGAGCTTACATATGTTTGGATTAGACTCT 1639
Qy 1321 TAAAATCCTTTGCCAAAATAAGGGATGTCAAAATATATGAAACATGTCCTTTAGAAAAATT 1380
Db 1640 TAAAATCCTTTGCCAAAATAAGGGATGTCAAAATATATGAAACATGTCCTTTAGAAAAATT 1699
Qy 1381 AGGAGATAAATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGTCTCTCTTA 1440
Db 1700 AGGAGATAAATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGTCTCTCTTA 1759
Qy 1441 AAGAAAGCATCTTGATATATTAATAAATCAAAAGATGAGGCTTCTTACATATACATCTTAG 1500
Db 1760 AAGAAAGCATCTTGATATATTAATAAATCAAAAGATGAGGCTTCTTACATATACATCTTAG 1819
Qy 1501 TTGATTATTAATAAAGGAAAAAGGTTTCCAGAGAAAAAGGCCAATACCTTAAGCATTTTTC 1560
Db 1820 TTGATTATTAATAAAGGAAAAAGGTTTCCAGAGAAAAAGGCCAATACCTTAAGCATTTTTC 1879
Qy 1561 CATGAGAAGCACTGCATACCTTACCTATGTGGAATTAATCAATTTTATGCAATTTTGTGAGG 1620
Db 1880 CATGAGAAGCACTGCATACCTTACCTATGTGGAATTAATCAATTTTATGCAATTTTGTGAGG 1939
Qy 1621 CATAATAATATAAGTGCTTTTAGAAATTAATCAATTTTATGCAATTTTGTGAGG 1680
Db 1940 CATAATAATATAAGTGCTTTTAGAAATTAATCAATTTTATGCAATTTTGTGAGG 1999
Qy 1681 CATCCTTATTAATTAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTATATATAGTC 1740
Db 2000 CATCCTTATTAATTAACACCTATCTCAAAAACCTTACTTAGAAGGTTTTTATATATAGTC 2059
Qy 1741 CTACAAAAGACAAATGTATAAGCTGTAACAGAAATTTGAATTTTCTTTGCAAAACCC 1800
Db 2060 CTACAAAAGACAAATGTATAAGCTGTAACAGAAATTTGAATTTTCTTTGCAAAACCC 2119
Qy 1801 CTCCACAAAAGCAAAATCCTTTCAAGAATGGCATGGGCAATCTGTATGAACCTTTCCAGAT 1860
Db 2120 CTCCACAAAAGCAAAATCCTTTCAAGAATGGCATGGGCAATCTGTATGAACCTTTCCAGAT 2179

QY 1861 GGTGTTCAAGTGAAGATGTGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACATCGAC 1920
Db |||||
2180 GGTGTTCAAGTGAAGATGTGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACATCGAC 2239
QY 1921 GTAACTGGAAACCG 1934
Db |||||
2240 GTAACTGGAAACCG 2253

RESULT 3

US-09-457-066-36
; Sequence 36, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-09-457-066-36

Query Match 77.1%; Score 1491.8; DB 4; Length 1882;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1507; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 60
Db |||||
370 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 429
QY 61 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAA 120
Db |||||
430 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAA 489
QY 121 ACACGGATACAGCTAGTGTGTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180
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490 ACACGGATACAGCTAGTGTGTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 549
QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 240
Db |||||
550 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 609
QY 241 CGATGGTGTGGACACAAAGGAAGTTCTCCAAGGATAAAATCAAGAACGAACCAAAATAAA 300
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610 CGATGGTGTGGACACAAAGGAAGTTCTCCAAGGATAAAATCAAGAACGAACCAAAATAAA 669
QY 301 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 360
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670 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 729
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730 TTGCTGGAAGATTTCCAAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 789
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850 GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 909
QY 541 CCAGAGTCATGGCAAGAAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
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910 CCAGAGTCATGGCAAGAAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 969
QY 601 AGGTATACCATGACCCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
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970 AGGTATACCATGACCCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 1029
QY 661 CGTTACAGTTGCACTCCAGGAATTAATCTCGGTCAATATAAGAGAAAGAGCTGAAGTTGGCC 720
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1030 CGTTACAGTTGCACTCCAGGAATTAATCTCGGTCAATATAAGAGAAAGAGCTGAAGTTGGCC 1089
QY 721 AATGTGGTCTTCTTTCCACGTTGCCCTCCTCGTCAGCGCTGTGGAGGAAATTTGGCTGT 780
Db |||||
1090 AATGTGGTCTTCTTTCCACGTTGCCCTCCTCGTCAGCGCTGTGGAGGAAATTTGGCTGT 1149
QY 781 GGAACCTGTCAACTGGAGGTCTGTGCACATGCAATTCAGGGGAAAAACCGTGAAAAAGTATCAT 840
Db |||||
1150 GGAACCTGTCAACTGGAGGTCTGTGCACATGCAATTCAGGGGAAAAACCGTGAAAAAGTATCAT 1209
QY 841 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 900
Db |||||
1210 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 1269
QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTTGTATCTGCGCTCAAGACCA 960
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1270 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTTGTATCTGCGCTCAAGACCA 1329
QY 961 CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020
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1330 CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1389
QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAACTTACTACTAGCCTGCAATGCA 1080
Db |||||
1390 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAACTTACTACTAGCCTGCAATGCA 1449
QY 1081 ATGAACACAAAGTGGTGTGAGTCTCAGCCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1140
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1450 ATGAACACAAAGTGGTGTGAGTCTCAGCCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1509
QY 1141 GGTATATCATCAACTTCTATACCTTAAGAAATATAGGATTCGATTTAATAATAGTGTAG 1200
Db |||||
1510 GGTATATCATCAACTTCTATACCTTAAGAAATATAGGATTCGATTTAATAATAGTGTAG 1569
QY 1201 GTTATATATGCACAAAACACACACAGAAATATATTCATGTCTATGTGTATATAGATCAAA 1260
Db |||||
1570 GTTATATATGCACAAAACACACACAGAAATATATTCATGTCTATGTGTATATAGATCAAA 1629
QY 1261 G-----TTTTTTTTTGGTATATATAACCCAGGTACACCAGAGCTTACATATGTTGAGTTAGA 1316
Db |||||
1630 GTTTTTTTTTTTTTTGGTATATATAACCCAGGTACACCAGAGTTACATATGTTGAGTTAGA 1689
QY 1317 CTCTTAAAAATCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAA 1376
Db |||||
1690 CTCTTAAAAATCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAAA 1749
QY 1377 ATTTAGGAGATAAATTTTAAATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGCTCT 1436
Db |||||
1750 ATTTAGGAGATAAATTTTAAATTTTAAATTTTGAACACGAAAAACAATTTTGAATCTTGCTCT 1809
QY 1437 CTTAAAGAAAGCACTTGTATATTAAAAATCAAAAGATGAGGCTTTCTTACATATACATC 1496
Db |||||
1810 CTTAAAGAAAGCACTTGTATATTAAAAATCAAAAGATGAGGCTTTCTTACATATACATC 1869
QY 1497 TTAGTTGATTAAT 1509
Db |||||
1870 TTAGTTGATTAAT 1882

RESULT 4
US-09-540-224-1
; Sequence 1, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-09-540-224-1

Query Match 77.1%; Score 1491.8; DB 4; Length 1882;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1507; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAGGAAACGGCTACGTGCAGAGTCCTAGA 60
DB 370 TTGTACCGAAGAGATGAGACCATCCAGGTGAAGGAAACGGCTACGTGCAGAGTCCTAGA 429

QY 61 TTCCCGAACAGTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACCTCAGGAGAAAT 120
DB 430 TTCCCGAACAGTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACCTCAGGAGAAAT 489

QY 121 ACACGGATACAGCTAGTGTGTTGACAATCAGTTTGGATTAGAGGAAGCAGAAATGATATC 180
DB 490 ACACGGATACAGCTAGTGTGTTGACAATCAGTTTGGATTAGAGGAAGCAGAAATGATATC 549

QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 240
DB 550 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 609

QY 241 CGATGGTGTGGACACACAGGAAGTTCTCCCAAGGATAAAATCAAGAACGACCAAAATTA 300
DB 610 CGATGGTGTGGACACACAGGAAGTTCTCCCAAGGATAAAATCAAGAACGACCAAAATTA 669

QY 301 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 360
DB 670 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 729

QY 361 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 420
DB 730 TTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 789

QY 421 TCTATTTTCAGGGGTATCCTATAAATCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
DB 790 TCTATTTTCAGGGGTATCCTATAAATCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 849

QY 481 GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 540
DB 850 GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAAT 909

QY 541 CCAGAGTCATGGCAAGAGATCTTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
DB 910 CCAGAGTCATGGCAAGAGATCTTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 969

QY 601 AGGTACATACCATGACCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
DB 970 AGGTACATACCATGACCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 1029

QY 661 CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC 720
DB 1030 CGTTACAGTTGCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC 1089

QY 721 AATGTGTCTTCTTTCCACGTTGCTCTCGTGCAGCGCTGTGGAGGAAATTTGTGGCTGT 780
DB 1090 AATGTGTCTTCTTTCCACGTTGCTCTCGTGCAGCGCTGTGGAGGAAATTTGTGGCTGT 1149

QY 781 GGAACCTGCAACTGGAGGTCCTGCACATGCAATTCAGGGGAAACCCGTGAAAAAGTATCAT 840
DB 1150 GGAACCTGCAACTGGAGGTCCTGCACATGCAATTCAGGGGAAACCCGTGAAAAAGTATCAT 1209

QY 841 GAGGTATTACAGTTTGGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900
DB 1210 GAGGTATTACAGTTTGGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 1269

QY 901 CTAGTTGACATCCAGTTGGATCCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 960
DB 1270 CTAGTTGACATCCAGTTGGATCCATGAACGATGCGATTGTATCTGCAGCTCAAGACCA 1329

QY 961 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAAGGA 1020
DB 1330 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAAGGA 1389

QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACAGCAACCAAACTTACTACTAGCCTGCAATGCA 1080
DB 1390 GGGTGAGATAAGAGACCCCTTTTCTACAGCAACCAAACTTACTACTAGCCTGCAATGCA 1449

QY 1081 ATGAACACAAAGTGGTGTGCTGAGTCTCAGCCTTGTCTTGTAAATGCCATGGCAAGTAGAAA 1140
DB 1450 ATGAACACAAAGTGGTGTGCTGAGTCTCAGCCTTGTCTTGTAAATGCCATGGCAAGTAGAAA 1509

QY 1141 GGTATATCATCAACTTCTATACCTAAGAATATAGGATTGCAATTAATAGTTTGTAG 1200
DB 1510 GGTATATCATCAACTTCTATACCTAAGAATATAGGATTGCAATTAATAGTTTGTAG 1569

QY 1201 GTTATATATGCAAAAAACACACACAGAAATATATTCATGTCTATGTATATAGATCAAAAT 1260
DB 1570 GTTATATATGCAAAAAACACACACAGAAATATATTCATGTCTATGTATATAGATCAAAAT 1629

QY 1261 G-----TTTTTTTTTGGTATATATAACCCAGGTACACAGAGCTTACATATGTTGAGTTAGA 1316
DB 1630 GTTTTTTTTTTTTTTGGTATATATAACCCAGGTACACAGAGCTTACATATGTTGAGTTAGA 1689

QY 1317 CTCTTAAATTCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGCTTTTAGAAA 1376
DB 1690 CTCTTAAATTCCTTTGCCAAAAATAAGGGATGGTCAAAATATATGAAACATGCTTTTAGAAA 1749

QY 1377 ATTAGGAGATAAATTTATTTTAAATTTTAAATTTTAAACACAAAAACAATTTTGAATCTTGCTCT 1436
DB 1750 ATTAGGAGATAAATTTATTTTAAATTTTAAATTTTAAACACAAAAACAATTTTGAATCTTGCTCT 1809

QY 1437 CTTAAAGAAAGCATCTTGATATATTAAAAATCAAAAAGATGAGGCTTTCTTACATATACATC 1496
DB 1810 CTTAAAGAAAGCATCTTGATATATTAAAAATCAAAAAGATGAGGCTTTCTTACATATACATC 1869

QY 1497 TTAGTTGATTATT 1509
DB 1870 TTAGTTGATTATT 1882

RESULT 5
US-09-564-595D-1
; Sequence 1, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03

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; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-09-564-595D-1

Query Match      77.1%; Score 1491.8; DB 4; Length 1882;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1507; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTTAGA 60
Db 370 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTTAGA 429

QY 61 TTCCCGAACAGTACCCCGAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAAT 120
Db 430 TTCCCGAACAGTACCCCGAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAAT 489

QY 121 ACAGGATACAGCTAGTGTGGAAGTTGAAGATATATCCGAAACCGAGTACGAGAAATGATATC 180
Db 490 ACAGGATACAGCTAGTGTGGAAGTTGAAGATATATCCGAAACCGAGTACGAGAAATGATATC 549

QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCGAGTACGAGAAATGATATC 240
Db 550 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCGAGTACGAGAAATGATATC 609

QY 241 CGATGGTGTGGACACAAAGGAAGTTCCTCCAAGGATAAAATCAAGAACGAAACCAAAATAAA 300
Db 610 CGATGGTGTGGACACAAAGGAAGTTCCTCCAAGGATAAAATCAAGAACGAAACCAAAATAAA 669

QY 301 ATCATATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTTATTATTCT 360
Db 670 ATCATATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTTATTATTCT 729

QY 361 TTGCTGGAAGATTTCCAAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTACAAAGC 420
Db 730 TTGCTGGAAGATTTCCAAACCCGAGCAGCTTCAGAGACCAACTGGGAATCTGTACAAAGC 789

QY 421 TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAAACCGATCCCACTCTGATGCGGGAT 480
Db 790 TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAAACCGATCCCACTCTGATGCGGGAT 849

QY 481 GCTCTGGACAAAAAAATTCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT 540
Db 850 GCTCTGGACAAAAAAATTCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT 909

QY 541 CCAGAGTCATGGCAAGAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
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QY 601 AGGTACATACCATGACCCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
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QY 661 CGTTACAGTTGCACCTCCAGGAATTTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 720
Db 1030 CGTTACAGTTGCACCTCCAGGAATTTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 1089

QY 721 AATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTTGGGCTGT 780
Db 1090 AATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTTGGGCTGT 1149
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781 GGAACCTGTCAACTGGAGGTCTTGCAATGCAATGCAATTCAGGGAAAAACCGTGAATAAGTATCAT 840
Db 1150 GGAACCTGTCAACTGGAGGTCTTGCAATGCAATGCAATTCAGGGAAAAACCGTGAATAAGTATCAT 1209

QY 841 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 900
Db 1210 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 1269

QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATCGGATTGTATCTGCAGCTCAAGACCA 960
Db 1270 CTAGTTGACATCCAGTTGGATCACCATGAACGATCGGATTGTATCTGCAGCTCAAGACCA 1329

QY 961 CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020
Db 1330 CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1389

QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1080
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QY 1081 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAAATGCCAAGTAGAAA 1140
Db 1450 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAAATGCCAAGTAGAAA 1509

QY 1141 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCAATTTAATAATAGTTTGAG 1200
Db 1510 GGTATATCATCAACTTCTATACCTAAGAAATATAGGATTGCAATTTAATAATAGTTTGAG 1569

QY 1201 GTTATATATGCACAAAACACACACAGAAATATATTTCATGTCTATGTGTATATAGATCAAAT 1260
Db 1570 GTTATATATGCACAAAACACACACAGAAATATATTTCATGTCTATGTGTATATAGATCAAAT 1629

QY 1261 G-----TTTTTTTTTGGTATATATAACCGAGGTACACAGAGCTTACATATGTTTGAGTTAGA 1316
Db 1630 GTTTTTTTTTTTTGGTATATATAACCGAGGTACACAGAGCTTACATATGTTTGAGTTAGA 1689

QY 1317 CTCTTAAAAATCCTTTGCCAAAATAAGGGATGGTCAAATATATGAAACAATGCTCTTTAGAAA 1376
Db 1690 CTCTTAAAAATCCTTTGCCAAAATAAGGGATGGTCAAATATATGAAACAATGCTCTTTAGAAA 1749

QY 1377 ATTAGGAGATAAAATTTATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGCTCT 1436
Db 1750 ATTAGGAGATAAAATTTATTTTAAATTTTGAACACAAAAACAATTTTGAATCTTGCTCT 1809

QY 1437 CTTAAAGAAAAGCATCTTGATATATTAAAAATCAAAAAGATGAGGCTTTCTTACATATACATC 1496
Db 1810 CTTAAAGAAAAGCATCTTGATATATTAAAAATCAAAAAGATGAGGCTTTCTTACATATACATC 1869

QY 1497 TTAGTTGATTATT 1509
Db 1870 TTAGTTGATTATT 1882

RESULT 6
US-09-706-968-36
; Sequence 36, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 36
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-09-706-968-36

Query Match      77.1%; Score 1491.8; DB 4; Length 1882;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1507; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 60
Db 370 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 429

QY 61 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 120
Db 430 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 489

QY 121 ACACGGATACAGCTAGTGTGTTTGACAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180
Db 490 ACACGGATACAGCTAGTGTGTTTGACAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 549

QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 240
Db 550 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTATTAGAGGA 609

QY 241 CGATGGTGTGACACAAAGGAAGTTCCCTCCAAGGATAAAATCAAGAACGAACCAAAATTAAA 300
Db 610 CGATGGTGTGACACAAAGGAAGTTCCCTCCAAGGATAAAATCAAGAACGAACCAAAATTAAA 669

QY 301 ATCACATTCAAGTCCGATGACTACTTTTGGCTAAACCTGGATTCAAGATTATTATTCT 360
Db 670 ATCACATTCAAGTCCGATGACTACTTTTGGCTAAACCTGGATTCAAGATTATTATTCT 729

QY 361 TTGCTGGAAGATTTCCAACCCGACGAGCTTTCAGAGACCAACTGGGAATCTGTCAACAAGC 420
Db 730 TTGCTGGAAGATTTCCAACCCGACGAGCTTTCAGAGACCAACTGGGAATCTGTCAACAAGC 789

QY 421 TCTATTTCAGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
Db 790 TCTATTTCAGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 849

QY 481 GCTCTGGACAAAAAAATTGCAGAAATTTGTATACAGTGAAGATCTGTCTCAAGTACTTCAAT 540
Db 850 GCTCTGGACAAAAAAATTGCAGAAATTTGTATACAGTGAAGATCTGTCTCAAGTACTTCAAT 909

QY 541 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 910 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 969

QY 601 AGGTACATACCATGACCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGCCAAG 660
Db 970 AGGTACATACCATGACCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGCCAAG 1029

QY 661 CGTTACAGTTGCACTCCAGGAATTAATCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 720
Db 1030 CGTTACAGTTGCACTCCAGGAATTAATCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 1089

QY 721 AATGTGGTCTTTTCCACGTTGGCTCCTGTCAGCGCTGTGGAGGAAATTTGTGGCTGT 780
Db 1090 AATGTGGTCTTTTCCACGTTGGCTCCTGTCAGCGCTGTGGAGGAAATTTGTGGCTGT 1149

QY 781 GGAACGTGCACTGAGGCTCTGCACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 840
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QY 841 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTTAAGACCATGGCT 900
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QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATCGATTGTATCTGCAGCTCAAGACCA 960
Db 1270 CTAGTTGACATCCAGTTGGATCACCATGAACGATCGATTGTATCTGCAGCTCAAGACCA 1329

QY 961 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020
Db 1330 CCTCGATAAGAGAAATGTGCACATCCTTACATTAAAGCCTGAAAGAACCTTTAGTTTAAGGA 1389

QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1080
Db 1390 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCA 1449

QY 1081 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGTCTTTGTTAATGCCATGGCAAGTAGAAA 1140
Db 1450 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGTCTTTGTTAATGCCATGGCAAGTAGAAA 1509

QY 1141 GGTATATCATCAACTTCTATACCTAAAGAAATATAGGATTGCAATTAATAATAGTTTGTAG 1200
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Db 1690 CTCCTTAAATCCTTTGCCAAAATAAGGGATGGTCAAATATATGAACATGTCTTTAGAAA 1749

QY 1377 ATTTAGGAGATAAAATTTATTTTAAATTTTGAACACAAAACAATTTTGAATCTTGCTCT 1436
Db 1750 ATTTAGGAGATAAAATTTATTTTAAATTTTGAACACAAAACAATTTTGAATCTTGCTCT 1809

QY 1437 CTTAAAGAAAGCATCTTGATATATTAAAAATCAAAGATGAGGCTTTCTTACATATACATC 1496
Db 1810 CTTAAAGAAAGCATCTTGATATATTAAAAATCAAAGATGAGGCTTTCTTACATATACATC 1869

QY 1497 TTAGTTGATTATT 1509
Db 1870 TTAGTTGATTATT 1882

RESULT 7
US-09-808-972-1
; Sequence 1, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1882
; TYPE: DNA
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-002-185

Query Match      51.9%; Score 1003.4; DB 4; Length 1162;
Best Local Similarity 99.9%; Pred. No. 1.1e-253;
Matches 1004; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGAGAGTCCTAGA 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
158 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGAGAGTCCTAGA 217
Qy 61 TTCCCGAACAGCTACCCAGGAACCTGCTCTGACATGGCGGCTTCACTCTCAGGAGAAT 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
218 TTCCCGAACAGCTACCCAGGAACCTGCTCTGACATGGCGGCTTCACTCTCAGGAGAAT 277
Qy 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
278 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 337
Qy 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTTATAGAGGA 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
338 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTTATAGAGGA 397
Qy 241 CGATGGTGTGGACACAAGGAAGTTCCCTCCAAGGATAAAATCAAGAACCGAACCAAAATAAA 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
398 CGATGGTGTGGACACAAGGAAGTTCCCTCCAAGGATAAAATCAAGAACCGAACCAAAATAAA 457
Qy 301 ATCACATTCAGTCCGATGACTACTTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
458 ATCACATTCAGTCCGATGACTACTTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCT 517
Qy 361 TTGCTGGAAGATTTCCAAACCCGAGCAGCTTTCAGAGACCAACTGGGAATCTGTCAACAAGC 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
518 TTGCTGGAAGATTTCCAAACCCGAGCAGCTTTCAGAGACCAACTGGGAATCTGTCAACAAGC 577
Qy 421 TCTATTTCAGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
578 TCTATTTCAGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 637
Qy 481 GCTCTGGACAAAAAATTCAGAAATTTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
638 GCTCTGGACAAAAAATTCAGAAATTTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 697
Qy 541 CCAGAGTCATGGCAAGAAGATCTTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
698 CCAGAGTCATGGCAAGAAGATCTTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 757
Qy 601 AGGTCATACCATGACCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
758 AGGTCATACCATGACCGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 817
Qy 661 CGTTACAGTTGCACTCCAGGAATTAATCTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 720
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
818 CGTTACAGTTGCACTCCAGGAATTAATCTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 877
Qy 721 AATGTGGTCTTCTTTCCACGTTGCTCCTCGTCGACGCGCTGTGGAGGAATTTGTGGCTGT 780
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
878 AATGTGGTCTTCTTTCCACGTTGCTCCTCGTCGACGCGCTGTGGAGGAATTTGTGGCTGT 937
Qy 781 GGAAGTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 840
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
938 GGAAGTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 997
Qy 841 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
998 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 1057
Qy 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCGCTCAAGACCA 960
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1058 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCGCTCAAGACCA 1117
Qy 961 CCTCGATAAGAGAAATGTGCACATCTTTACATTAAAGCCTGAAAGAA 1005
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| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1118 CCTCGATAAGAGAATGTGCACATCCTTACATTAAAGCCTGAGAGAA 1162

RESULT 9
US-09-540-224-3
; Sequence 3, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
US-09-540-224-3

Query Match      41.1%; Score 795.4; DB 4; Length 1472;
Best Local Similarity 78.7%; Pred. No. 5.1e-199;
Matches 1007; Conservative 0; Mismatches 226; Indels 46; Gaps 3;

Qy 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGAGAGTCCTAGA 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
237 TTGTACCGAAGAGAGAGGAACAATTCAGGTGACAAGCAATGGCCATGTGCGAGAGTCCTCGC 296
Qy 61 TTCCCGAACAGCTACCCAGGAACCTGCTCTGACATGGCGGCTTCACTCTCAGGAGAAT 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
297 TTCCCGAACAGCTACCCAGGAACCTGCTCTGACATGGTGGTCCGTTCCCAGGAGAAA 356
Qy 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
357 ACACGGATACAACTGTCTTTGACCATCAATTCGGACTAGAGGAAGCAGAAAAATGACATT 416
Qy 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATTTATAGAGGA 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
417 TGTAGGTATGACTTTGTGGAAGTTGAAGAGTCTCAGAGAGCAGCACTGTTGTGAGAGGA 476
Qy 241 CGATGGTGTGGACACAAGGAAGTTCCCTCAAGGATAAAATCAAGAACCGAACCAAAATAAA 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
477 AGATGGTGTGGCCACAAGGAGATCCCTCCAAGGATAACGTCAAGAACAAACAGATTAAA 536
Qy 301 ATCACATTCAAGTCCGATGACTACTTTTGGCTAAACCTGGATTCAAGATTTATTATTCT 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
537 ATCACATTAAAGTCTGATGACTACTTTTGGCAAAAACCTGGATTCAAGATTTATTATTCA 596
Qy 361 TTGCTGGAGAGATTTCCAAACCCGAGCAGCTTTCAGAGACCAACTGGGAATCTGTCACAAGC 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
597 TTTGTGGAAGATTTCCAAACCCGGAAGCAGCCTCAGAGACCAACTGGGAATCAGTCACAAGC 656
Qy 421 TCTATTTTCAGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
657 TCTTTTCTCTGGGTGTCCTATCACTCTCCATCAATAACGGACCCCACTCTCACTGCTGAT 716
Qy 481 GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGAGAGATCTGCTCAAGTACTTCAAT 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
717 GCCCTGGACAAAAACTGTGCGAGAAATTCGATACCGTGGAGAGATCTACTTAAGCACTTCAAT 776
Qy 541 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
777 CCAGTGTCTTGGCAAGATGATCTGGAGAAATTTGTATCTGGACACCCCTCATATAGAGGC 836
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QY 601 AGGTCATACCAGACCGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
837 AGGTCATACCATGATCGAAGTCCAAAAGTGGACCTGGACAGGCTCAATGATGATCAAG 896
QY 661 CGTTACAGTTGCACCTCCAGGAATTAAGTCCGTCATATAAAGAGAGAGCTGAAGTTGGCC 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
897 CGTTACAGTTGCACCTCCAGGAATCACTCTGTGAACCTCAGGGAGGAGCTGAAGCTGACC 956
QY 721 AATGTGGTCTTCTTTCCACGTTGCCCTCCTCGTGCAGCGCTGTGGAGGAAATTTGGCTGT 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
957 AATGCAGTCTTCTTCCACGATGCCCTCCTCGTGCAGCGCTGTGGTGGCAACTGTGGTTGC 1016
QY 781 GGAACGTGCAACTGGAGTCCCTGCACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1017 GGAACGTGCAACTGGAGTCCCTGCACATGCAGCTCAGGGAAGACAGTGAAGAGTATCAT 1076
QY 841 GAGGTATTACAGTTTGAGCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1077 GAGGTATTGAAGTTTGAGCTGGACATTTCAAGAGAGAGGGGCAAGCTAAGAAATATGGCT 1136
QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACCGATGCGATGCGATTTGATCTGCAGCTCAAGACCA 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1137 CTGTGTGATATCCAGCTGGATCATCATGAGCGATGTGACTGTATCTGCAGCTCAAGACCA 1196
QY 961 CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAAGGA 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1197 CCTCGATAAAACACTATGCACATCTGTACTTTGATTATGAAAGGACCTTTAGGTTA--- 1252
QY 1021 GGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCCAACTTACTACTAGCCTGCAATGCA 1080
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1253 -----CAAAAACCCTAAGAAGCTTCTAATCTCAGTGCA 1285
QY 1081 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1140
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1286 ATGAATGCATATGG-----AAATGTTGCTTTGTTAGTGCCATGGCAAGAAG 1334
QY 1141 GGTATATCATCAACTTCTATACCTAAGAATATAGGATGCAATTAATAATAGTTTGAG 1200
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1335 CAAATATCATTAATTTCTATATACATAAAACATAGGAATTCACATTATCAATAGTATGTGAA 1394
QY 1201 GTTATATATGCACAAACACACAGAAATATATTCATGTCTATGTATATAGATCAAAAT 1260
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1395 GATATGTATATATACTTATATACATGACTAGCTCTATG----TATGTAATATAGATTAAT 1450
QY 1261 GTTTTTTTTGGTATATATA 1279
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1451 ACTTATTTCAGTATATTTA 1469

RESULT 10
US-09-564-595D-52
; Sequence 52, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
US-09-564-595D-52

Query Match 41.1%; Score 795.4; DB 4; Length 1472;
Best Local Similarity 78.7%; Pred. No. 5.1e-199;
Matches 1007; Conservative 0; Mismatches 226; Indels 46; Gaps 3;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAAGAAACGGCTACGTGACAGATCCTAGA 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
237 TTGTACCGAGAGAGAGAAACATTCAGGTGACAAGCAATGGCCATGTGACAGATCCTCGC 296
QY 61 TTCCCGAACAGCTACCCAGGAACCTGCTCCTGACATGCGGGCTTCACTCTCAGGAGAAT 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
297 TTCCCGAACAGCTACCCAAAGGAACCTGCTTCTGACATGGTGGCTCCGTTCCCAGGAGAAA 356
QY 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
357 ACACGGATACAACTGTCTTTGACCATCAATTCGGACTAGAGGAAGCAGAAAATGACATT 416
QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCCAGTACCATATTAGAGGA 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
417 TGTAGGTATGACTTTGTGGAAGTTGAAGAGTCTCAGAGAGCAGCACTGTTGTGAGAGGA 476
QY 241 CGATGGTGTGGACACAAGGAAGTTTCTCCAAAGGATAAAATCAAGAACGAAACCAAAATATAA 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
477 AGATGGTGTGGCCACAAGGAGATCCCTCCAGGATAACGTCAGGAACAAACAGATATAA 536
QY 301 ATCACAATTCAGTCCGATGACTACTTTTGTGGTAAACCTGGATTCAAGATTTATTATTCT 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
537 ATCACAATTTAAGTCTGATGACTACTTTTGTGGGAAAACCTGGATTCAAGATTTATTATCA 596
QY 361 TTGCTGGAAGATTTCCAAACCCGACGAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
597 TTTGTGGAAGATTTCCAAACCCGGAAGCAGCCTCAGAGACCAACTGGGAATCACTCAACAAGC 656
QY 421 TCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAAACGGATCCCACCTCGATTGCGGAT 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
657 TCTTTCTCTGGGGTGTCTATCACTCTCCATCAATAACGGAACCCCACTCTCACTGCTGAT 716
QY 481 GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
717 GCCCTGGACAAAACCTGTCGAGAAATTCGATACCGTGGAAAGATCTACTTAAAGCACTTCAAT 776
QY 541 CCAGAGTCAATGCGCAAGAAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
777 CCAGTGTCTTGGCAAGATGATCTGGAGAAATTTGTATCTGGACACCCCTCATTTATAGAGGC 836
QY 601 AGGTCAATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
837 AGGTCAATACCATGATCGGAAGTCCAAAGTGGACCTGGACAGGCTCAATGATGATGTCAAG 896
QY 661 CGTTACAGTTGCACCTCCAGGAATTAAGTCCGTCATATAAAGAGAGAGCTGAAGTTGGCC 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
897 CGTTACAGTTGCACCTCCAGGAATCACTCTGTGAACCTCAGGGAGGAGCTGAAGCTGACC 956
QY 721 AATGTGGTCTTCTTTCCACGTTGCCCTCCTCGTGCAGCGCTGTGGAGGAAATTTGGCTGT 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
957 AATGCAGTCTTCTTCCACGATGCTCCTCGTGCAGCGCTGTGGTGGCAACTGTGGTTGC 1016
QY 781 GGAACGTGCAACTGGAGGTCTTGACATGCAATTCAGGGAAAAACCGTGAAAAAGTATCAT 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1017 GGAACGTGCAACTGGAGGTCTTGACATGCAATTCAGGGAAAGACAGTGAAGAAAGTATCAT 1076
QY 841 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACATGGCT 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1077 GAGGTATTGAAGTTTGAGCCTGGACATTTCAAGAGAAAGGGGCAAAAGCTAAGAAATATGGCT 1136
QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTTGATCTGCAGCTCAAGACCA 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1137 CTGTTGATATCCAGCTGGATCATCATGAGCGGATGTGACTGTATCTGCAGCTCAAGACCA 1196

QY 1261 GTTTTTTTGGTATATATA 1279
Db 1451 ACTTTATTTCAGTATATTTA 1469

RESULT 12
US-09-564-595D-6
; Sequence 6, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence
; NAME/KEY: misc feature
; LOCATION: (1)-(1110)
; OTHER INFORMATION: n = A,T,C or G
US-09-564-595D-6

Query Match 36.1%; Score 697.6; DB 4; Length 1110;
Best Local Similarity 56.9%; Pred. No. 2.2e-173;
Matches 549; Conservative 259; Mismatches 157; Indels 0; Gaps 0;

QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCTTAGA 60
Db 145 YTNAYMGNMGNGAYGARACNATHCARGTNAARGGNAAYGGNTAYGTNCARWSNCCNMGN 204

QY 61 TTCCGGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 120
Db 205 TTYCCNAAAYWSNTAYCCNMGNAAAYTYNTYTNACNTGGMGNYTNCAYWSNCARGARAAY 264

QY 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTGGATTAGAGGAAGCAGAAAATGATATC 180
Db 265 ACNMGNATHCARYTNGTNTTYGAYAAAYCARTTYGGNYTNGARGGARGCNGARAAYATH 324

QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACAGTACCATTATTAGAGGA 240
Db 325 TGYMGNAYGAYTTYGTNGARGTNGARGAYATHWSNGARACNWSNACNATHATHMNGNGN 384

QY 241 CGATGGTGTGGACACAAGGAAGTTCTCCTCAAGGATAAAATCAAGAACGAAACCAAAATPAAA 300
Db 385 MGNLTGGTGYGNCAYARGARTNCCNMGNATHAARWSNMGNAACNAAAYCARATHAAR 444

QY 301 ATCAGATTCAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 360
Db 445 ATHACNTTYAARWSNGAYGAYTAYTYGTNGCNAAARCCNGGNTTYAARATHAYTAYWSN 504

QY 361 TTGCTGGAAGATTTCCAAACCCGACGAGCTTCAGAGACCAACTGGGAATCTGTCCACAGC 420
Db 505 YTYNTNGARGAYTTYCARCCNGCNGCNGCNGCNGARACNAAAYTGGGARWSNGTNACNWSN 564

QY 421 TCTATTTACGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
Db 565 WSNATHWSNGGNGTNSNTAYAAAYWSNCCNWSNGTNACNGAYCCNACNYTNATHGCGNAY 624

QY 481 GCTCTGGACAAAAAATTGCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT 540
Db 625 GCNYTNGAYAAARAATHGCGARTTYGAYACNGTNGARGAYTYNTYNTAARTAYTTYAAY 684

QY 541 CCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGC 600
Db 685 CCNGARWSNTGGCARGARGAYTNGARAAYATGTAYYTNNGAYACNCCNMGNTAYMNGNGN 744

QY 601 AGGTACATACCATGACCGGAAGTCAAAAAGTTGACCTGGATAGGTCAATGATGATGCCAAG 660
Db 745 MGNWSNTAYCAYGAYMGNAAARWSNAARGTNGAYYTNNGAYMGNYNAAAYGAYGCGNAAR 804

QY 661 CGTTACAGTTGCACCTCCAGGAATTTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 720
Db 805 MGNAYWSNTGYACNCCNMGNAAAYTAYWSNGTNAAYATHMNGARGARYTNAARYTNGCN 864

QY 721 AATGTGGTCTTTTCCACGTTTGCCTCTCCTCGTGACGCGCTGTGGAGGAAAATTTGTGGCTGT 780
Db 865 AAYGTNGTNTTYTCCNMGNTGYTYNTYNTGTNCARMGNTGYGGNGNAAYTYGGNTGY 924

QY 781 GGAACCTGTCAACTGGAGGTCCTGCACATGCAATTGAGGGAACCCGTGAAAAAGTATCAT 840
Db 925 GGNACNGTNAAYTGGMGNWSNTGYACNTGYAAYWSNGNAARACNGTNAARAARTAYCAY 984

QY 841 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900
Db 985 GARGTNTNCARTTYGARCCNGNCAYATHAARMGNMGNMGNMGNMGNMGNMGNMGNMGN 1044

QY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATCGGATTGTATCTGCAGCTCAAGACCA 960
Db 1045 YTNGTNGAYATHCARYTNGAYCAYCAYGARMGNTGYGAYTGYATHTYGWSNWSNMGNGCN 1104

QY 961 CCTCG 965
Db 1105 CCNMG 1109

RESULT 13
US-09-438-046-3
; Sequence 3, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-438-046-3

Query Match 34.2%; Score 662; DB 4; Length 690;
Best Local Similarity 98.4%; Pred. No. 3.9e-164;
Matches 679; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 366 GGAAGATTTCACACCCGACGAGCTTCAGAGACCAACTGGGAATCTGTCACAAGCTCTAT 425
|||||
Db 1 GGAAGATTTCACACCCGACGAGCTTCAGAGACCAACT-GGAATCTGTCACAAGCTCTGT 59

QY 426 TTCAGGGGTATCCCTATAACTCTCCATCAGTAACGGATCCCACCTCTGATTGGGATGCTCT 485
|||||
Db 60 TTCAGGGTATCCCTATAACTCTCCATCAGTAACGGATCCCACCTCTGATTGGGATGCTCT 119

QY 486 GGACAAAAAATTGCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAATCCAGA 545
|||||
Db 120 GGACAAAAAATTGCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAATCCAGA 179

QY 546 GTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTC 605
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Db 180 GTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTC 239

QY 606 ATACCATGACCGGAAGTCAAAAGTTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTA 665
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Db 240 ATACCATGACCGGAAGTCAAAAGTTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTA 299

QY 666 CAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAAGAGCTGAAGTTGGCCAAATGT 725
|||||
Db 300 CAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAAGAGCTGAAGTTGGCCAAATGT 359

QY 726 GGTCTTCTTCCACGTTGCCTCCTCGTGACGCGTGTGGAGGAAATTTGGTGTGGAAAC 785
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Db 360 GGTCTTCTTCCACGTTGCCTCCTCGTGACGCGTGTGGAGGAAATTTGGTGTGGAAAC 419

QY 786 TGTCAACTGGAGGTCCTGACATGCAATTCAGGGAACCCGTTGAAAAAGTATCATGAGGT 845
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Db 420 TGTCAACTGGAGTCTCTGACATGCAATTCAGGGAACCCGTTGAAAAAGTATCATGAGGT 479

QY 846 ATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCCATGGCTCTAGT 905
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Db 480 ATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCCATGGCTCTAGT 539

QY 906 TGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCAACCTCG 965
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Db 540 TGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCAACCTCG 599

QY 966 ATAAGAGAAATGTGCATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAAGAGGGTG 1025
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Db 600 ATAAGAGAAATGTGCATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAAGAGGGTG 659

QY 1026 AGATAAGAGACCCCTTTTCTTACCAGCAACC 1055
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Db 660 AGATAAGAGACCCCTTTTCTTACCAGCAACC 689

RESULT 14
US-09-438-046-1
; Sequence 1, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; EARLIER FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10

; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-438-046-1

Query Match 18.4%; Score 355.2; DB 4; Length 360;
Best Local Similarity 99.2%; Pred. No. 1.1e-83;
Matches 357; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 769 AATTGTGGCTGTGGAACCTGTCAACTGGAGTCTCTGCACATGCAATTCAGGGAAAAACCGTG 828
|||||
Db 1 AATTGTGGCTGTGGAACCTGTCAACTGGAGTCTCTGCACATGCAATTCAGGGAAAAACCGTG 60

QY 829 AAAAAAGTATCATGAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGAGGGGTAGAGCT 888
|||||
Db 61 AAAAAAGTATCATGAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGAGGGGTAGAGCT 120

QY 889 AAGACCATGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGC 948
|||||
Db 121 AAGACCATGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGC 180

QY 949 AGCTCAAGACCACTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCT 1008
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Db 181 AGCTCAAGACCACTCGATAAGAGAAATGTGCACATCCTTACATTAAGCCTGAAAGAACCA 240

QY 1009 TTAGTTTAAAGGAGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAAACTTACTACTA 1068
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Db 241 TTAGTTTAAAGGAGGTGAGATAAGAGACCCCTTTTCTACCAGCAACCAAGACTTACTACTA 300

QY 1069 GCCTGCAATGCAATGAACACAAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCAT 1128
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Db 301 GCCTGCAATGCAATGAACACAAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCAT 360

RESULT 15
US-09-222-575-13/c
; Sequence 13, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Human
US-09-222-575-13

Query Match 11.1%; Score 213.8; DB 3; Length 256;
Best Local Similarity 94.0%; Pred. No. 1.2e-46;
Matches 234; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

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Db 256 TTGAATCTTGTTCTTTTAAAGAACATTTTGTATATTGAAAATCAAAAAGATGAGGCTTT 197
QY 1483 CTTACATATACATCTTAGTTGATTATTAAAAAGGAAAAA ---GGTTTCCAGAGAAAAGG 1539
Db 196 TTAACATATACATTTTAGTTGATTATTAAAAAGGAAAAATATGGTTTCCAGAGAAAAGG 137
QY 1540 CCAATACCTAAGCATTTTTCATGAGAGCACTGCATACCTTACCTATGTGGACTGTAAT 1599
Db 136 CCAATACCTAAGCATTTTTCATGAGAGCACTGCATACCTTACCTATGTGGACTGTAAT 77
QY 1600 AACCTGTCTCCAAAACCATGCCATAATAATAAGTGCTTTAGAAAATTAAATCATTGTGT 1659
Db 76 AACCTGTCTCCAAAACCATGCCATAATAATAAGTGCTTTAGAAAATTAAATCATTGTGT 17
QY 1660 TTTTATGC 1668
Db 16 TTTTATGC 8

Search completed: October 31, 2004, 09:10:12
Job time : 190 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:51:22 ; Search time 5506 Seconds
(without alignments)
12799.572 Million cell updates/sec

Title: US-10-086-623-5
Perfect score: 1934
Sequence: 1 ttgtaccgaagagatgagac.....atcgacgtaactggaacccg 1934

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1: *
2: gb_est2: *
3: gb_htc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1913.2 | 98.9 | 3739 | 3 | AF113216 Homo sapi |
| 2 | 967.4 | 50.0 | 1095 | 9 | AY419997 Homo sapi |
| 3 | 962.2 | 49.8 | 1095 | 9 | AY419998 Pan trogl |
| 4 | 832.4 | 43.0 | 1797 | 3 | AK003359 Mus muscu |
| 5 | 748.2 | 38.7 | 1095 | 9 | AY419999 Mus muscu |
| 6 | 632.2 | 32.7 | 686 | 5 | BU616629 UI-H-DF0- |
| 7 | 621.8 | 32.2 | 687 | 5 | BU616664 UI-H-DF0- |
| 8 | 596.2 | 30.8 | 606 | 5 | BQ575044 UI-H-EZ1- |
| 9 | 524.6 | 27.1 | 580 | 5 | BU685336 UI-CF-DU1 |
| 10 | 523.6 | 27.1 | 799 | 2 | BE914552 601665653 |
| 11 | 510.8 | 26.4 | 560 | 2 | AW968905 EST380981 |
| 12 | 503.2 | 26.0 | 508 | 1 | AL600063 DKFZp313A |
| 13 | 499.8 | 25.8 | 819 | 5 | BU359805 603477657 |
| 14 | 490.4 | 25.4 | 723 | 4 | BI689894 603310727 |
| 15 | 484.6 | 25.1 | 505 | 2 | AW274723 xn34b02.x |
| 16 | 483.6 | 25.0 | 985 | 5 | BU311960 603405535 |
| 17 | 483.6 | 25.0 | 1044 | 5 | BU213231 603106994 |
| 18 | 482 | 24.9 | 485 | 1 | AA488996 aa54c10.8 |
| 19 | 477.2 | 24.7 | 727 | 5 | BU326159 603493350 |
| 20 | 473 | 24.5 | 480 | 5 | BU431765 UI-HF-BN0 |
| 21 | 455 | 23.5 | 798 | 5 | BU404150 603482511 |
| 22 | 434.4 | 22.5 | 969 | 6 | CD242494 AGENCOURT |
| 23 | 428.4 | 22.2 | 554 | 7 | CO603983 DG8-274a2 |
| 24 | 423.8 | 21.9 | 811 | 5 | BU326859 603489249 |

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| C 25 | 420.4 | 21.7 | 551 | 7 | CO596606 | CO596606 | DG8-130i1 |
| C 26 | 413.8 | 21.4 | 467 | 4 | BM144799 | BM144799 | TCAAP1D13 |
| C 27 | 412.8 | 21.3 | 774 | 5 | BU290871 | BU290871 | 603607294 |
| C 28 | 411.2 | 21.3 | 645 | 5 | BU402438 | BU402438 | 603483558 |
| C 29 | 407.8 | 21.1 | 533 | 7 | CO612657 | CO612657 | DG9-116n1 |
| C 30 | 404.6 | 20.9 | 532 | 7 | CO611691 | CO611691 | DG9-107b5 |
| C 31 | 392 | 20.3 | 533 | 7 | CO658472 | CO658472 | DG34-2023 |
| C 32 | 387.2 | 20.0 | 921 | 5 | BU315557 | BU315557 | 603488052 |
| C 33 | 386.8 | 20.0 | 406 | 1 | AI221902 | AI221902 | qg99h07.x |
| C 34 | 383 | 19.8 | 613 | 5 | BU312449 | BU312449 | 603544305 |
| C 35 | 355.2 | 18.4 | 360 | 1 | AA488780 | AA488780 | aa54c10.r |
| C 36 | 350.6 | 18.1 | 655 | 7 | CO699403 | CO699403 | DG32-158p |
| C 37 | 345.6 | 17.9 | 455 | 7 | CO600294 | CO600294 | DG8-1C24 |
| C 38 | 335 | 17.3 | 761 | 7 | CN078301 | CN078301 | EC2BBA14D |
| C 39 | 328.8 | 17.0 | 633 | 6 | CF135616 | CF135616 | UI-HF-BN0 |
| C 40 | 323 | 16.7 | 609 | 2 | AW503454 | AW503454 | UI-HF-BN0 |
| C 41 | 322 | 16.6 | 579 | 5 | BU407817 | BU407817 | 603483546 |
| C 42 | 304 | 15.7 | 529 | 5 | BU251898 | BU251898 | 603404337 |
| C 43 | 295.6 | 15.3 | 318 | 1 | AA904948 | AA904948 | oj81b10.s |
| C 44 | 293.4 | 15.2 | 317 | 1 | AA736766 | AA736766 | oa23a03.s |
| C 45 | 292.8 | 15.1 | 762 | 5 | BU384694 | BU384694 | 603858418 |

ALIGNMENTS

RESULT 1
AF113216
LOCUS AF113216 3739 bp mRNA linear HTC 12-APR-2002
DEFINITION Homo sapiens MSTP036 mRNA, complete cds.
ACCESSION AF113216
VERSION AF113216.1 GI:11640579
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3739)
AUTHORS Liu, B., Liu, Y.Q., Wang, X.Y., Zhao, B., Sheng, H., Zhao, X.W., Liu, S., Xu, Y.Y., Ye, J., Song, L., Gao, Y., Zhang, C.L., Zhang, J., Wei, Y.J., Cao, H.Q., Zhao, Y., Liu, L.S., Ding, J.F., Gao, R.L., Wu, Q.Y., Qiang, B.Q., Yuan, J.G., Liew, C.C., Zhao, M.S. and Hui, R.T.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu, Beijing 100037, P.R. China
FEATURES
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/db_xref="taxon:9606"
/tissue_type="aorta"
107..1219
/codon_start=1
/product="MSTP036"
/protein_id="AAG39287.1"
/db_xref="GI:11640580"
/translation="MHRLIFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES
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EAENDICRYDFEVEDISETTIIRGWCGHKVPPIKSRNQIKITPKSDDYFVAK
PGFKIYSLLEDQFPAASETNSWESVTSSISGVSNPSPTDPTLLADALDKKIAEFD
TVEDILKYFNPESQEDLENMYLDTPRYGRSYHDKRSKVOLDRLNDDAKRSYCTPRN
YSVNIREEELKLANVFFPRCLLVQRCGNGCGGTNWRSRCTNSGKTVKKYHEVLQFE
PGHIKRRGRAKTMALVDIQLDHHERCDCICSSRRPPR"

| | | | | |
|-----------------------|--------------|---|------------|--------------|
| Query Match | 98.9% | Score 1913.2; | DB 3; | Length 3739; |
| Best Local Similarity | 99.7% | Pred. No. 0; | | |
| Matches 1928; | Conservative | 0; | Mismatches | 3; |
| | | | Indels | 3; |
| | | | Gaps | 1; |
| QY | 1 | TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTACGTGCAGAGTCTCTAGA | 60 | |
| | | | | |
| Db | 251 | TTGTACCGAAGAGATGAGACCATCCAGGTGAAGAAACGGCTACGTGCAGAGTCTCTAGA | 310 | |

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Db 311 TTCCGGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 370
QY 121 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC 180
Db 371 ACACGGATACAGCTAGTGTGTTGACAAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATC 430
QY 181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAACCCAGTACCAATTATTAGAGGA 240
Db 431 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAACCCAGTACCAATTATTAGAGGA 490
QY 241 CGATGGTGTGGACACAGGAAGTTCTCCAAAGGATAAAATCAAGAACCGAACCAAAATTA 300
Db 491 CGATGGTGTGGACACAGGAAGTTCTCCAAAGGATAAAATCAAGAACCGAACCAAAATTA 550
QY 301 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 360
Db 551 ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTATTATTCT 610
QY 361 TTGCTGGAAGATTTCCAAACCCGACGAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 420
Db 611 TTGCTGGAAGATTTCCAAACCCGACGAGCTTCAGAGACCAACTGGGAATCTGTCAACAAGC 670
QY 421 TCTATTTCAGGGGTATCCTATPAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGAT 480
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QY 481 GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGAGATCTGCTCAAGTACTTCAAT 540
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QY 721 AATGTGCTCTTCTTTCCAGTGTGCTCCTCGTGACGCGCTGTGGAGGAAATTTGTGCTGT 780
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QY 781 GGAATGTCAACTGGAGGTCCTGCACATGCAATTCAGGGGAAAACCGTGAAAAAGTATCAT 840
Db 1031 GGAATGTCAACTGGAGGTCCTGCACATGCAATTCAGGGGAAAACCGTGAAAAAGTATCAT 1090
QY 841 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 900
Db 1091 GAGGTATTACAGTTTGAGCCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCT 1150
QY 901 CTAGTTTGACATCCAGTTGGATCACCATGAACGATGCGATTGATCTGCAGCTCAAGACCA 960
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QY 1021 GGGTGAGATAAGAGACCCCTTTTCTTACCAGCAACCAACTTACTAGCTGCAATGCA 1080
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QY 1081 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1140
Db 1331 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAGAAA 1390

QY 1141 GGTATATCATCAACTTCTATATACCTAAGAAATATAGGATTGGCATTTAATAATAGTGTGAG 1200
Db 1391 GGTATATCATCAACTTCTATATACCTAAGAAATATAGGATTGGCATTTAATAATAGTGTGAG 1450
QY 1201 GTTATATATGCACAAAACACACACAGAAAATATATTCAATGTCTATGTATATAGATCAAAAT 1260
Db 1451 GTTATATATGCACAAAACACACACAGAAAATATATTCAATGTCTATGTATATAGATCAAAAT 1510
QY 1261 GTTTTTTTTGGTATATATAAACCGGTACACAGAGCTTACATATGTGTTGAGTTAGACTCT 1320
Db 1511 GTTTTTTTTGGTATATATAAACCGGTACACAGAGCTTACATATGTGTTGAGTTAGACTCT 1570
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Db 1631 AGGAGATAAAATTTATTTTAAATTTTGAAAACACAAAACAATTTTGAATCTTGCTCTCTTA 1690
QY 1441 AAGAAAGCATCTTGATATATTAAAAATCAAAAAGATGAGGCTTTCTACATATACATCTTAG 1500
Db 1691 AAGAAAGCATCTTGATATATTAAAAATCAAAAAGATGAGGCTTTCTACATATACATCTTAG 1750
QY 1501 TTGATTATTAAAAAAGGAAAAA --GGTTTCCAGAGAAAAGGCCAATACCTAAGCATTTT 1557
Db 1751 TTGATTATTAAAAAAGGAAAAAATATGGTTTCCAGAGAAAAGGCCAATACCTAAGCATTTT 1810
QY 1558 TTCCATGAGAAGCACTGCATACCTTACCTATGTGGACTGTAATAACCTGTCTCCAAAACCA 1617
Db 1811 TTCCATGAGAAGCACTGCATACCTTACCTATGTGGACTATAATAACCTGTCTCCAAAACCA 1870
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QY 1738 GTCCTACAAAAGCAATGTATAAGCTGTAAACAGAAATTTTGAATGTTTTTCTTGTGCAAAA 1797
Db 1991 GTCCTACAAAAGCAATGTATAAGCTGTAAACAGAAATTTTGAATGTTTTTCTTGTGCAAAA 2050
QY 1798 CCCCTCCACAAAAGCAAAATCCTTTCAAGATGGCATGGGCATTTCTGTATGAACCTTTCCA 1857
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Db 2111 GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTTGAAAACATC 2170
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Db 2171 GACGTAACCTGGAAA 2184

RESULT 2
AY419997
LOCUS
DEFINITION Homo sapiens HCM7077 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY419997
VERSION AY419997.1 GI:39775954
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1095)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

TITLE Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1095)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
gene <1..>1095
/locus_tag="HCM7077"
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Best Local Similarity 99.9%; Pred. No. 7.5e-218;
Matches 968; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 60
Db 127 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 186
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QY 181 TGTAGGTATGATTTGTGGAAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGA 240
Db 307 TGTAGGTATGATTTGTGGAAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGA 366
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QY 481 GCTCTGGACAAAAAATTCAGAAATTTGATACAGTGGAAAGATCTGCTCAAGTACTTCAAT 540
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Db 1087 CCTCGATAA 1095
RESULT 3
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DEFINITION genomic survey sequence.
ACCESSION AY419998
VERSION AY419998.1 GI:39775955
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 - (bases 1 to 1095)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1095)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene <1..>1095
/locus_tag="HCM7077"
ORIGIN
Query Match 49.8%; Score 962.2; DB 9; Length 1095;
Best Local Similarity 99.5%; Pred. No. 1.3e-216;
Matches 964; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 60
Db 127 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 186
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QY 121 |ACACGGATACAGCTAGTGTGTTTGACAATCAGTTTGGATTAGAGGAAGCAGAAAAATGATATC 180

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Db 907 |GGAACGTCAACTGGAGGTCCTGCACATGCAATTTCAGGGAACCCGTGAAAAAGTATCAT 966

QY 841 |GAGGTATTACAGTTTGAAGCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 900

Db 967 |GAGGTATTACAGTTTGAAGCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACCATGGCT 1026

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Db 1087 |CCTCGATAA 1095

RESULT 4

AK003359

LOCUS

DEFINITION

AK003359

VERSION

KEYWORDS

AK003359

Mus musculus 18-day embryo whole body cDNA, RIKEN full-length

enriched library, clone:1110003109 product:platelet-derived growth

factor D mRNA, full insert sequence.

AK003359

AK003359.2 GI:26382601

HTC; CAP trapper.

1797 bp mRNA linear HTC 03-APR-2004

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 1797)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,

Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,

Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,

Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,

Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,

Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,

Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,

Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,

Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,

Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,

Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,

URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,

Fax:81-45-503-9216)

On Dec 10, 2002 this sequence version replaced gi:12833975.

Please visit our web site (<http://genome.gsc.riken.jp/>) for further

details.

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues. First strand cDNA was primed with a primer

[5' GAGAGAGAGCGCGCAACTCGAGTTTTTTTTTTTTT 3'], cDNA was

prepared by using trehalose thermo-activated reverse transcriptase

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

genomic survey sequence.
AY419999
VERSION AY419999.1 GI:39775956
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1095)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1095)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source Location/Qualifiers
1..1095
/organism="Mus musculus"
/mol_type="genomic DNA"
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gene <1..>1095
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ORIGIN
Query Match 38.7%; Score 748.2; DB 9; Length 1095;
Best Local Similarity 85.8%; Pred. No. 5.7e-166;
Matches 831; Conservative 0; Mismatches 138; Indels 0; Gaps 0;
QY 1 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 60
Db 127 TTGTACCAGAGAGAGGAGAAATTCAGGTGACAAGCAATGGCCATGTGCAGAGTCCTCGC 186
QY 61 TTCCGGAACAGCTACCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAAT 120
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Db 1087 CCTCGATAA 1095

RESULT 6
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UI-H-DF0-ben-f-24-0-UI 3', mRNA sequence.
ACCESSION BU616629
VERSION BU616629.1 GI:23282844
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 686)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
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POLYA=Yes.
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/tissue_type="Subchondral Bone"
/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_DF0"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC.
TAG_TISSUE=subchondral bone
TAG_LIB=UI-H-DF0
TAG_SEQ=GTTAAGCGTC"

ORIGIN

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|-----------------------|------|--|--------------|--------|------------|----|--------|------|
| Query Match | | 32.7%; | Score | 632.2; | DB | 5; | Length | 686; |
| Best Local Similarity | | 98.7%; | Pred. | No. | 1.5e-138; | | | |
| Matches | | 660; | Conservative | 0; | Mismatches | 3; | Indels | 6; |
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| Db | 686 | CTTTAGTTTAAGGAGGTGAGATAAGAGACCCCTTTCTCTACCAGCAACCAAACTTACTAC | 627 | | | | | |
| QY | 1067 | TAGCCTGCAATGCAATGAACACAAGTGGTTCGTGAGTCTCAGCCTTGCTTTGTTAATGCC | 1126 | | | | | |
| Db | 626 | TAGCCTGCAATGCAATGAACACAAGTGGTTCGTGAGTCTCAGCCTTGCTTTGTTAATGCC | 567 | | | | | |
| QY | 1127 | ATGGCAAGTAGAAAAGGTATATCATCAACTTCTATACCTAAAGATATAGGATTGCATTAA | 1186 | | | | | |
| Db | 566 | ATGGCAAGTAGAAAAGGTATATCATCAACTTCTATACCTAAAGATATAGGATTGCATTAA | 507 | | | | | |
| QY | 1187 | TAATAGTGTGTTGAGGTTATATATGCACAAACACACAGAGAAATATATTCATGCTATGTG | 1246 | | | | | |
| Db | 506 | TAATAGTGTGTTGAGGTTATATATGCACAAACACACAGAGAAATATATTCATGCTATGTG | 447 | | | | | |
| QY | 1247 | TATATAGATCAAAATG---TTTTTTTGGTATATATAACCAAGGTACACCAGGTTTACATA | 1303 | | | | | |
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| QY | 1304 | TGTTTGAGTTAGACTCTTAAAAATCCTTTGCCAAATAAAGGGATGGTCAAAATATATGAAAC | 1363 | | | | | |
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| Db | 326 | ATGTCTTTAGAAAATTAGGAGATAAAATTTATTTTAAATTTTGAAACACACGAAACAATTT | 267 | | | | | |
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| Db | 206 | TTACATATACATCTTAGTTGATTATTAAAAAAGGAAAAATATGGTTTCCAGAGAAAAGGC | 147 | | | | | |
| QY | 1541 | CAATACCTAAGCATTTTTCATGAGAAGCACTGCATCTTACCTATGTGGACTGTAATA | 1600 | | | | | |
| Db | 146 | CAATACCTAAGCATTTTTCATGAGAAGCACTGCATCTTACCTATGTGGACTGTAATA | 87 | | | | | |
| QY | 1601 | ACCTGTCTCCAAAACCATGCCATAATAATATAAGTCTTTAGAAATTAATCATTTGTGTT | 1660 | | | | | |
| Db | 86 | ACCTGTCTCCAAAACCATGCCATAATAATATAAGTCTTTAGAAATTAATCATTTGTGTT | 27 | | | | | |
| QY | 1661 | TTTTATGCA | 1669 | | | | | |
| Db | 26 | TTTTATGCA | 18 | | | | | |

RESULT 7
BU616664/c
LOCUS
DEFINITION
UI-H-DF0-ben-p-22-0-UI.s1 NCI CGAP DF0 Homo sapiens cDNA clone
UI-H-DF0-ben-p-22-0-UI 3', mRNA sequence.
ACCESSION
BU616664
VERSION
BU616664.1 GI:23282879
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 687)
REFERENCE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 284-304, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
1..687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-DF0-ben-p-22-0-UI"
/tissue_type="Subchondral Bone"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_DF0"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC.
TAG_TISSUE=subchondral bone
TAG_LIB=UI-H-DF0
TAG_SEQ=GTTAAGCGTC"

ORIGIN

| | | | | | | | | |
|-----------------------|------|--|--------------|--------|------------|----|--------|------|
| Query Match | | 32.2%; | Score | 621.8; | DB | 5; | Length | 687; |
| Best Local Similarity | | 98.5%; | Pred. | No. | 4.2e-136; | | | |
| Matches | | 660; | Conservative | 0; | Mismatches | 3; | Indels | 7; |
| | | | | | | | Gaps | 3; |
| QY | 1007 | CTTTAGTTTAAGGAGGTGAGATAAGAGACCCCTTTCTCTACCAGCAACCAAACTTACTAC | 1066 | | | | | |
| Db | 687 | CTTTAGTTTAAGGAGGTGAGATAAGAGACCCCTTTCTCTACCAGCAACCAAACTTACTAC | 628 | | | | | |
| QY | 1067 | TAGCCTGCAATGCAATGAACAC-AAGTGGTTCGTGAGTCTCAGCCTTGCTTTGTTAATGC | 1125 | | | | | |
| Db | 627 | TAGCCTGCAATGCAATGAACACAAAGTGGTTCGTGAGTCTCAGCCTTGCTTTGTTAATGC | 568 | | | | | |
| QY | 1126 | CATGGCAAGTAGAAAAGGTATATCATCAACTTCTATACCTTAAGAATATAGGATTGCATTTA | 1185 | | | | | |
| Db | 567 | CATGGCAAGTAGAAAAGGTATATCATCAACTTCTATACCTTAAGAATATAGGATTGCATTTA | 508 | | | | | |

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QY 1186 ATAATAGTGTGGTTATATATATGCACAAACACACAGAAATATATTCATGCTATGT 1245
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
507 ATAATAGTGTGGTTATATATATGCACAAACACACAGAAATATATTCATGCTATGT 448
QY 1246 GTATATAGATCAAAATG---TTTTTTTTTGGTATATATAAACAGGTACACCAGAGCTTACAT 1302
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
447 GTATATAGATCAAAATGTTTTTTTTTGGTATATATAAACAGGTACACCAGAGGTACAT 388
QY 1303 ATGTTTGAGTTAGACTCTTAAAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAA 1362
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
387 ATGTTTGAGTTAGACTCTTAAAAATCCTTTGCCAAAATAAGGGATGGTCAAAATATATGAAA 328
QY 1363 CATGCTTTAGAAAATTTAGGAGATAAATTTATTTTAAATTTTGAAACACAAAACAATT 1422
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
327 CATGCTTTAGAAAATTTAGGAGATAAATTTATTTTAAATTTTGAAACACCGAAACAATT 268
QY 1423 TTGAATCTTGCTCTCTTAAAGAAAGCATCTTGATATATAAAAAATCAAAAGATGAGGCTTT 1482
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
267 TTGAATCTTGCTCTCTTAAAGAAAGCATCTTGATATATAAAAAATCAAAAGATGAGGCTTT 208
QY 1483 CTTACATATACATCTTAGTTGATTTATAAAAAAGGAAAAA---GGTTTCCAGAGAAAAGG 1539
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
207 CTTACATATACATCTTAGTTGATTTATAAAAAAGGAAAAATATGGTTTCCAGAGAAAAGG 148
QY 1540 CCAATACCTAAGCATTTTTTCCATGAGAAAGCACTGCATTAACCTATGTGGACTGTAAT 1599
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
147 CCAATACCTAAGCATTTTTTCCATGAGAAAGCACTGCATTAACCTATGTGGACTGTAAT 88
QY 1600 AACCTGTCTCCAAAACCATGCATATAATAATAGTGCTTTAGAAAATTAATCATTTGTGT 1659
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
87 AACCTGTCTCCAAAACCATGCATAATAATAAGTGCTTTAGAAAATTAATCATTTGTGT 28
QY 1660 TTTTATGCA 1669
Db |||||||
27 TTTTATGCA 18

RESULT 8
BQ575044/c
LOCUS BQ575044 606 bp mRNA linear EST 19-JUN-2002
DEFINITION UI-H-EZ1-bbd-o-15-0-UI.s1 NCI CGAP_Ch2 Homo sapiens cDNA clone
UI-H-EZ1-bbd-o-15-0-UI 3', mRNA sequence.
ACCESSION BQ575044
VERSION BQ575044.1 GI:21478361
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 606)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopaedics
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-24, >AT rich#Low complexity 122-142,
>AT rich#Low complexity 249-325, >(TA)n#simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1..606
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source
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/clone="UI-H-EZ1-bbd-o-15-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ch2"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCACGCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ1
TAG_SEQ=ATCTAATATG"

ORIGIN
Query Match 30.8%; Score 596.2; DB 5; Length 606;
Best Local Similarity 99.5%; Pred. No. 4.7e-130;
Matches 598; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 922 CACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAAATGTGCAC 981
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
606 CACCATGAACGATGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAAATGTGCAC 547
QY 982 ATCCTTACATTAAAGCCTGAAAGAACCTTTAGTTTAAAGGAGGTGAGATAAGAGACCCTTT 1041
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
546 ATCCTTACATTAAAGCCTGAAAGAACCTTTAGTTTAAAGGAGGTGAGATAAGAGACCCTTT 487
QY 1042 TCCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCAATGAACACAAAGTGGTTGCTGA 1101
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
486 TCCTACCAGCAACCAAACTTACTACTAGCCTGCAATGCAATGAACACAAAGTGGTTGCTGA 427
QY 1102 GTCTCAGCCTTGCTTTGTTTAATGCCATGGCAAGTAGAAAGGTATATCATCAACTCTATA 1161
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
426 GTCTCAGCCTTGCTTTGTTTAATGCCATGGCAAGTAGAAAGGTATATCATCAACTCTATA 367
QY 1162 CCTAAGAATATAGGATTGCATTTAATAATAGTGTGTTGAGGTTATATATGCACAAACACAC 1221
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
366 CCTAAGAATATAGGATTGCATTTAATAATAGTGTGTTGAGGTTATATATGCACAAACACAC 307
QY 1222 ACAGAAATATATTCATGTCATGTGTATATAGATCAAAATGTTTTTTTGGTATATATAAC 1281
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
306 ACAGAAATATATTCATGTCATGTGTATATAGATCAAAATGTTTTTTTGGTATATATAAC 247
QY 1282 CAGGTACACCAGAGCTTACATATGTTTGAGTTAGACTCTTAAATCCTTTGCCAAAATAA 1341
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
246 CAGGTACACCAGAGCTTACATATGTTTGAGTTAGACTCTTAAATCCTTTGCCAAAATAA 187
QY 1342 GGGATGGTCAAATATATGAACATGTCTTTTAGAAAATTTAGGAGATAAAATTTATTAA 1401
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
186 GGGATGGTCAAATATATGAACATGTCTTTTAGAAAATTTAGGAGATAAAATTTATTAA 127
QY 1402 ATTTTGAACACAAAACAATTTTGAATCTTGCTCTCTTAAAGAAAGCATCTTGTATATTA 1461
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
126 ATTTTGAACACAAAACAATTTTGAATCTTGCTCTCTTAAAGAAAGCATCTTGTATATTA 67
QY 1462 AAAATCAAAAGATGAGGCTTTCTTACATATACATCTTAGTTGATTATTAAGGAAAAA 1521
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
66 AAAATCAAAAGATGAGGCTTTCTTACATATACATCTTAGTTGATTATTAAGGAAAAA 7
QY 1522 A 1522
Db |
6 A 6
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RESULT 9
BU685336/c
LOCUS      BU685336               580 bp      mRNA      linear      EST 07-OCT-2002
DEFINITION UI-CF-DUI1-aav-f-05-0-UI.s2 UI-CF-DUI Homo sapiens cDNA clone
            UI-CF-DUI1-aav-f-05-0-UI 3' , mRNA sequence.
ACCESSION  BU685336
VERSION     BU685336.1   GI:23539180
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 580)
AUTHORS    Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
PUBMED      8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
            CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            The following repetitive elements were found in this cDNA
            sequence: 284-304, >AT-rich#Low_complexity (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.

FEATURES             Location/Qualifiers
     source           1..580
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-DUI1-aav-f-05-0-UI"
                     /tissue type="Primary Lung Epithelial Cells"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-DUI1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site 1: EcoR I; Site 2: Not I;
                     UI-CF-DUI1 is a normalized cDNA library containing the
                     following tissue(s): Primary Lung Epithelial Cells The
                     library was constructed according to Bonaldo, Lennon and
                     Soares, Genome Research, 6:791-806, 1996. First strand
                     cDNA synthesis was primed with an oligo-dT primer
                     containing a Not I site. Double stranded cDNA was ligated
                     to an EcoR I adaptor, digested with Not I, and cloned
                     directionally into pT7T3-Pac vector. The oligonucleotide
                     used to prime the synthesis of first-strand cDNA contains
                     a library tag sequence that is located between the Not I
                     site and the (dT)18 tail. The sequence tag for this
                     library is GGCTGTAGGC.
                     TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
                     TAG_LIB=UI-CF-DUI1
                     TAG_SEQ=GGCTGTAGGC"

ORIGIN
Query Match          27.1%; Score 524.6; DB 5; Length 580;
Best Local Similarity 98.2%; Pred. No. 4.1e-113;
Matches 553; Conservative 0; Mismatches 4; Indels 6; Gaps 2;

QY      1113  GCTTTGTTAATGCCATGCAAGTAGAAAGGTATATCATCAACTTCTATACCTAAGAATAT 1172
          ||||||| } ||||||| } ||||||| } ||||||| } ||||||| } ||||||| } ||||||| }
          ||||||| } ||||||| } ||||||| } ||||||| } ||||||| } ||||||| } ||||||| }

Db       580   GCTTTGTTAATCCCATGCAAGTAGAAAGGTATATCATCAACTTCTATACCTAAGAATAT 521

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RESULT 12
AL600063          508 bp      mRNA      linear      EST 04-SEP-2003
LOCUS             DKFZp313A2132.r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DEFINITION       DKFZp313A2132 5', mRNA sequence.
ACCESSION        AL600063
VERSION          AL600063.1 GI:15163351
KEYWORDS         EST.
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 508)
AUTHORS        Bloecker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and
                Wiemann,S.
TITLE          EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and
                Wiemann,S.)
JOURNAL        Unpublished (1999)
COMMENT        Contact: MIPS
                MIPS
                Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
                This is the 5' sequence of the clone insert
                Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                Braunschweig/Germany) within the cDNA sequencing consortium of the
                German Genome Project.
                No s1 sequence available.
                This clone (DKFZp313A2132) is available at the RZPD in Berlin.
                Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES             Location/Qualifiers
     source           1..508
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp313A2132"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="313 (synonym: hlcc2)"
                     /note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"

ORIGIN
Query Match      26.0%; Score 503.2; DB 1; Length 508;
Best Local Similarity 99.4%; Pred. No. 4.6e-108;
Matches 505; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 162 GGAAGCAGAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAC 221
      |||||||
Db 1 GGAAGCAAAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAC 60

QY 222 CAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGAAGTTCCTCCAGGATAAAATC 281
      |||||||
Db 61 CAGTACCATTGTTAGAGGACGATGGTGTGGACACAAGGAAGTTCCTCCAGGATAAAATC 120

QY 282 AAGAACGAACCAAAATTAAATCATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGG 341
      |||||||
Db 121 AAGAACGAACCAAAATTAAATCATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGG 180

QY 342 ATTCAGATTATTATTTCTTTGCTGGAAGATTTCCAACCCGACGAGCTTCAGAGACCAA 401
      |||||||
Db 181 ATTCAGATTATTATTTCTTTGCTGGAAGATTTCCAACCCGACGAGCTTCAGAGACCAA 240

QY 402 CTGGGAATCTGTCAAGCTCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGA 461
      |||||||
Db 241 CTGGGAATCTGTCACTAGCTCTATTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGA 300

QY 462 TCCCACTCTGATTGCGGATGCTCTGGACAAAAAAATTGCAGAATTTTGATACAGTGAAGA 521
      |||||||
Db 301 TCCCACTCTGATTGCGGATGCTCTGGACAAAAAAATTGCAGAATTTTGATACAGTGAAGA 360

QY 522 TCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAAGATCTTTGAGAAATATGTATCTGGA 581
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Db 361 TCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTATCTGGA 420
      |||||||
QY 582 CACCCCTCGGTATCGAGGCAGGTCAATACATGACCGGAAGTCAAAAGTTGACCTGGATAG 641
      |||||||
Db 421 CACCCCTCGGTATCGAGGCAGGTCAATACATGACCGGAAGTCAAAAGTTGACCTGGATAG 480
      |||||||
QY 642 GCTCAATGATGATGCCAAGCGTTACAGT 669
      |||||||
Db 481 GCTCAATGATGATGCCAAGCGTTACAGT 508
      |||||||

RESULT 13
BU359805          819 bp      mRNA      linear      EST 28-NOV-2002
LOCUS             603477657F1 CSEQCHN71 Gallus gallus cDNA clone CHEST363b15 5', mRNA
DEFINITION       sequence.
ACCESSION        BU359805
VERSION          BU359805.1 GI:25867806
KEYWORDS         EST.
SOURCE           Gallus gallus (chicken)
ORGANISM         Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE       1 (bases 1 to 819)
AUTHORS        Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
                Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
                A Comprehensive Collection of Chicken cDNAs
JOURNAL         Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE         22335534
PUBMED         12445392
COMMENT        Contact: Simon Hubbard
                Department of Biomolecular Sciences
                University of Manchester Institute of Science and Technology
                (UMIST)
                PO Box 88, Manchester, M60 1QD, UK
                Tel: 01612008930
                Fax: 01612360409
                Email: Simon.Hubbard@umist.ac.uk.

FEATURES             Location/Qualifiers
     source           1..819
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="White Leghorn, Hisex"
                     /db_xref="taxon:9031"
                     /clone="CHEST363b15"
                     /dev_stage="36"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN71"
                     /note="Organ: hearts; Vector: pBluescript II KS(+);
                     Site_1: EcoRI; Site_2: NotI; This normalized library was
                     constructed from 1 million independent clones. cDNA
                     synthesis was initiated using an oligo(dT) primer, using
                     methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."

ORIGIN
Query Match      25.8%; Score 499.8; DB 5; Length 819;
Best Local Similarity 79.6%; Pred. No. 3.3e-107;
Matches 617; Conservative 0; Mismatches 152; Indels 6; Gaps 2;

QY 91 CTGACATGGCGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTTCACAATCAG 150
      |||||||
Db 1 CTGACATGGCGCTGCACCTCCCCAGAGAGCACCAGGATCCAGCTGGCTTTTGATATATCAG 60
```

QY 151 TTTGGATTAGAGGAAGCAGAAAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGAT 210
Db 61 TTTGGACTGGAGGAGCCTGAAATATGATATCTGCAGGTATGACTTTGTGGAAGTGAAGAT 120
QY 211 ATATCCGAAACCAAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGAAGTTCTCTCA 270
Db 121 TTATCAGAGACCAGCACAGTTATACGAGGAAGTGGTGTGGGACACAAGGAAGTACCTCCA 180
QY 271 AGGATAAATCAAGAACGAACCAATTAATCAATTCAGTCCGATGACTACTTTGTG 330
Db 181 AGAATAACATCAAGAACAAATCAGATAAAGATAACCTTCAATCCGATGACTACTTTGTG 240
QY 331 GCTAAACCTGGATTCAAGATTTATTATTCTTTGCTGGAAAGATTTCCAAACCGCAGCAGCT 390
Db 241 GCTAAACCAAGATTCAAGATTTGTACTCCCTTGTGGATGATTTCCAGC--ATGCAGCC 297
QY 391 TCAGAGACCAACTGGGAATCTGTCAAGACTCTATTTTCAGGGGTATCCTATAACTCTCCA 450
Db 298 TCAGAAACCAACTGGGAATCAGTCACAAGCTCTGTCTCAGGGGTCTCCTATCCCTCTCCA 357
QY 451 TCAGTAACGGATCCCACTCTGATTGCGGATGCTCTGGACAAAAAATTCAGAAATTTGAT 510
Db 358 TCAGTGACCGACCCCTACACTCAGCAGAGAGCCCTGGATCAGACCAATTGCTGCATTGAC 417
QY 511 ACAGTGAAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAGATCTTCAGAAAT 570
Db 418 ACTGTGGAAGATCTGCTTAACACTTTAATCCAGACTCTCTGGAAGAGATCTCAGAAAT 477
QY 571 ATGTATCTGGACA---CCCCCTGGTATCGAGGCGAGGTATACCATGACCCGGAAGTCAAAA 627
Db 478 TTGTACACAGAAAGTGGCCACCATTATCGAGGCGAGGATACCATGACAGGAAGTCCAAA 537
QY 628 GTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACAGTTGCATCCCGAGGAATTAC 687
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QY 688 TCGTCAATATAAGAGAAGAGTGAAGTTGGCCAAATGTGGTCTTTTCCACGTTGCCTC 747
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RESULT 14
BI689894
LOCUS
DEFINITION BI689894 723 bp mRNA linear EST 18-SEP-2001
603310727F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5346438 5',
mRNA sequence.
ACCESSION BI689894
VERSION BI689894.1 GI:15652523
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 723)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1180 row: f column: 07
High quality sequence stop: 692.

FEATURES
source

Location/Qualifiers
1..723
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/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5346438"
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/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 25.4%; Score 490.4; DB 4; Length 723;
Best Local Similarity 86.1%; Pred. No. 5.4e-105;
Matches 589; Conservative 0; Mismatches 91; Indels 4; Gaps 4;
QY 154 GGATTAGAGGAAGCAGAAAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATA 213
Db 41 GGACTAGAGGAAGCAGAAAAATGACATTTGTAGGTATGACTTTGTGGAAGTTGAAGAGTC 100
QY 214 TCCGAAACCAAGTACCATTATTAGAGG-ACGATGGTGTGGACACAAGGAAGTTCTCTCCAAG 272
Db 101 TCAGAGAGCAGCACTGTTGTGAGAGGAACGATGGTGTGGCCACAAGGAGATCCCTCCAAG 160
QY 273 GATAAAATCAAGAACGAACCAAAATTAATAATCACATTCAAGTCCGATGACTACTTTGTGGC 332
Db 161 GATAACGTCAAGAACAAACCAGATTAAATACATTTAAGTCTGTGACTACTTTGTGGC 220
QY 333 TAAACCTGGATTCAAGATTTATTATTCTTTGCTGGAAGATTTCCAAACCGCAGCAGCTTC 392
Db 221 AAAACCTGGATTCAAGATTTATTATTCTTTGTTGGAAGATTTCCAAACCGGAAGCAGCCTC 280
QY 393 AGAGACCAACTGGGAATCTGTCAAGCTCTATTTCAGGGGTATCCTATAACTCTCCATC 452
Db 281 AGAGACCAACTGGGAATCAGTCACAGCTCTTTCTCTGGGTGTCTCTATCACTCTCCATC 340
QY 453 AGTAACGGATCCCACTCTGATTGCGGATGCTCTGGACAAAAAATTCAGAAATTTGATAC 512
Db 341 AATAACGGACCCCACTCTCACTGTCTGATGCCCTGGACAAAACCTGTCGAGAATTCGATAC 400
QY 513 AGTGAAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAGATCTTGAGAAATAT 572
Db 401 CGTGAAGATCTACTTAAGCACITTCATCCAGTGTCTTTGGCAAGATGATCTGGAGAAATTT 460
QY 573 GTATCTGGACACCCCTCGGTATCGAGGCAAGTCCATCCATGACCGGAAGTCAAAAGTTGA 632
Db 461 GTATCTGGACACCCCTCATTTATAGAGCAGGTCCATCCATGATCGGAAGTCCAAAGTGA 520
QY 633 -CCTGGATAGGCTCAATGATGATGCCAAGCGTTACAGTTGCATCCAGGAATTAATCTCGG 691
Db 521 CCCTGGACAGGCTCAATGATGATGTCAAGCGTTACAGTTGCATCCAGGAATCACTCTG 580
QY 692 TCAA-TATAAGAGAAAGAGCTGAAGTTGGCCAAATGTGGTCTTCTTTCCACGTTGCCCTC 750
Db 581 TGAACCCCTCAGGGAGGAGCTGAAGCTGACCAATGCAGTCTTCTTCCACGATGCCCTCCTC 640
QY 751 GTGACGCTGTGGAGGAATTTGTGGCTGTGGAACCTGTCAACTGGAGGTCTTGACATGC 810
Db 641 GTGACGCTGTGGTGGCAACTGTGTTGCGGAACGTGTC-ACTGGAAGTCTTGACATGC 699
QY 811 AATTGAGGAAACCGTGAAAAAG 834
Db 700 AGCTCAGGGAAGACAGTGAAGAG 723

RESULT 15
AW274723/c
LOCUS
DEFINITION xn34b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695563 3',
mRNA sequence.
ACCESSION AW274723
VERSION AW274723.1 GI:6661753
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 505)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 475.

FEATURES
source
1..505
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/db_xref="taxon:9606"
/clone="IMAGE:2695563"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

ORIGIN
Query Match 25.1%; Score 484.6; DB 2; Length 505;
Best Local Similarity 98.8%; Pred. No. 1.2e-103;
Matches 499; Conservative 0; Mismatches 4; Indels 2; Gaps 1;
QY 1007 CTTTAGTTTAAGGAGGTGAGATAAGAGACCCTTTTCCTACCAGCAACCAAACTTACTAC 1066
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Db 505 CTTTAGTTTAAGGAGGTGAGATAAGAGACCCTTTTCCTACCAGCAACCAAACTTACTAC 446
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QY 1067 TAGCCTGCAATGCAATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCC 1126
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Db 445 TAGCCTGCAATGCAATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCC 386
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QY 1127 ATGGCAAGTAGAAAGGTATATCATCAACTTCTATACCTAAGAATATAGGATGCATTAA 1186
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Db 385 ATGGCAAGTAGAAAGGTATATCATCAACTTCTATACCTAAGAATATAGGATGCATTAA 326
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QY 1187 TAATAGTGTTTGAGGTTATATATGCACAAACACACACAGAAATATATTCAATGCTATGTG 1246
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Db 325 TAATAGTGTTTGAGGTTATATATGCACAAACACACACAGAAATATATTCAATGCTATGTG 266
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QY 1247 TATATAGATCAAATG--TTTTTTTGGTATATATAACCAGGTACACCAGGCTTACATAT 1304
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Db 265 TATATAGATCAAATGTTTTTTTTTTGGTATATATAACCAGGTACACCAGAGGTTACATAT 206
QY 1305 GTTTGAGTTAGACTCTTAAATCCCTTTGCCAAAAATAAGGGATGGTCAATATATGAAACA 1364
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Db 205 GTTTGAGTTAGACTCTTAAATCCCTTTGCCAAAAATAAGGGATGGTCAATATATGAAACA 146
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QY 1365 TGTCCTTTAGAAAAATTTAGGAGATAAATTTTAAATTTTGAACACAAAAACAATTTT 1424
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Db 145 TGTCCTTTAGAAAAATTTAGGAGATAAATTTTAAATTTTGAACACGAAACAATTTT 86
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QY 1425 GAATCTTGCTCTCTTAAAGAAAGCATCTTGTATATTAAAAATCAAAGATGAGGCTTTCT 1484
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Db 85 GAATCTTGCTCTCTTAAAGAAAGCATCTTGTATATTAAAAATCAAAGATGAGGCTTTCT 26
QY 1485 TACATATACATCTTAGTTGATTATT 1509
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Db 25 TACATATACATCTTAGATGAATATT 1

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Job time : 5513 secs

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